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<p>(54) Title: HYBRID GROWTH FACTORS</p> <p>(57) Abstract</p> <p>The present invention provides recombinant hematopoietic molecules comprising at least a portion of a first hematopoietic molecule having early myeloid differentiation activity and at least a portion of a second hematopoietic molecule having late myeloid differentiation activity. Nucleic acid molecules encoding such recombinant molecules, as well as pharmaceutical compositions comprising such recombinant factors are also disclosed.</p>		

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HYBRID GROWTH FACTORSBACKGROUND OF THE INVENTION

5 Within this application several publications are referenced by Arabic numerals within parentheses. Full citations for these references may be found at the end of the specification immediately preceding the Sequence Listing. The disclosures of these publications in their entirety are hereby incorporated by reference into this application in
10 order to more fully describe the state of the art to which this invention pertains.

A variety of factors can influence the activity of a cell. Frequently a factor exerts its influence by interacting with a receptor on the
15 surface of a cell. After binding to the receptor, the signal which determines the cellular response to the factor can be mediated through a number of different events, including internalization of the factor or alterations of the receptor caused by ligand binding. During the course of hematopoietic differentiation, a number of different factors
20 are involved in the maturation of a pluripotent stem cell into a fully differentiated cell. The activities of these factors during the course of hematopoietic differentiation have resulted in these factors being characterized as early factors or late factors. For example, factors such as interleukin-3 (IL-3) and granulocyte-macrophage colony
25 stimulating factor (GM-CSF) are considered early factors, while erythropoietin (Epo), macrophage colony stimulating factor (M-CSF), and granulocyte colony stimulating factor (G-CSF) are considered late factors.

30 Based upon studies performed with purified factors and in vitro colony forming unit assays, it appears that both IL-3 and GM-CSF act on pluripotent cells before they become committed to a particular hematopoietic pathway. After the events stimulated by these factors are underway, such lineage restricted cells become receptive to
35 further differentiation mediated by such late factors as Epo, (which leads to the maturation of erythrocytes), G-CSF (which leads cells

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into the granulocytic pathway), and M-CSF (which leads to the maturation of macrophages). Experiments described in recent publications (1,2,3) have demonstrated in vitro that early or late factors alone are poor stimuli of colony formation. However, when an
5 early factor such as IL-3 or GM-CSF is combined with a late factor, levels of colony formation equivalent to that seen with conditioned media having full activity is observed. Thus, differentiation appears to be dependent upon the dual activities of early and late factors.

10 Despite a clear requirement for both IL-3 or GM-CSF and Epo for the formation of erythroid colony forming units, published results indicate that IL-3 can down-modulate high affinity Epo receptors (4). Because the amount of IL-3 required to demonstrate down-modulation of the Epo receptor was higher than that reported by others who
15 demonstrated functional full IL-3 activity in the presence of Epo, it is unclear whether this phenomenon is relevant in vivo.

Previous experiments in animals (22-26) suggest that under conditions of hematopoietic regeneration, optimal expansion of late progenitors
20 could only occur in the presence of an adequate early progenitor pool. This then makes manipulations that result in the expansion of early hematopoietic progenitor pools extremely desirable. IL-3 has been shown to exert a differentiative and proliferative effect on early progenitor cells and at IL-3 concentrations which had little or no
25 effect alone, Epo acted synergistically to induce proliferation and differentiation of erythroid progenitors. (27) By targeting a molecule with both early (IL-3) and late (Epo and G-CSF) activities to early progenitor cells, optimal expansion of a desired lineage should be possible.

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SUMMARY OF THE INVENTION

The present invention concerns hybrid molecules comprising early and late differentiation factors produced by genetic manipulation. By covalently linking such factors the local concentration of the late factor is very high at the surface of a cell to which the early factor is bound. Additionally, if down-modulation is relevant *in vivo*, binding of late factors to any remaining low-affinity receptors, e.g. Epo receptors, could be enhanced, thus reducing the amount of late factor required to stimulate the cell. Furthermore, by linking an early factor with a late factor, such early factor may act more specifically to stimulate only the desired lineage, thus reducing any undesirable effects mediated by the early factor. Finally, it is considerably easier to produce and administer to a patient a single factor with two activities rather it would to produce and administer two separate factors.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows a Western blot analysis of IL-3/Epo hybrid growth factors in CHO CM. CHO CM was collected from clones 23-10 (IL-3:Epo Flex), 5-4 (IL-3:Epo Short) and 17-3-1 (Epo:IL-3 Short). Hybrid growth factor concentrations were determined by ELISA assay. CM containing 74 ng of IL-3:Epo Flex (having a 23 aa flexible linker (lane 2), 73.5 ng of IL-3:Epo Short (having a short 2 aa linker) (lane 3), 80 ng of Epo:IL-3 Short (having a 3 aa linker) (lane 4) were subjected to SDS-PAGE (10-20% gel) electrophoresis and were assayed for Epo by Western blotting with a mouse anti-Epo polyclonal antisera as described in Example 7. Medium conditioned by CHO cells transfected with the vector pEe6 (lane 5) and rHu Epo 10 ng (lane 6), 20 ng (lane 7), 30 ng (lane 8), 70 ng (lane 9), and 100 ng (lane 10) were included. Molecular size markers in kilodaltons (lane 1).

Figure 2 shows AML193 cells proliferate in response to the IL-3 moiety of the hybrid growth factors. AML193 cells were grown to stationary phase and suspended in RPMI-1640 plus 10% FCS and growth

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factor deprived for 16 hours. The indicated concentrations of growth factors were added for 42 hours followed by a 6 hour pulse of (³H) thymidine as described in Example 7. NO GF (no growth factor); CHO CM (medium conditioned by CHO cells transfected with the vector pEe6); Epo (rHu Epo); IL-3 (rHu IL-3); IL-3:Epo Flex (CHO CM containing IL-3:Epo fusion protein with a 23aa flexible linker); IL-3:Epo Short (CHO CM containing IL-3:Epo fusion protein with a 2aa linker); Epo:IL-3 Short (CHO CM containing Epo:IL-3 fusion protein with a 3aa linker).

Figure 3 shows dose response of IL-3 adapted AML193 cells to the IL-3 moiety of the hybrid growth factors. IL-3 adapted AML 193 cells were grown to stationary phase and suspended in RPMI-1640 plus 10% FCS minus growth factor for 16 hours. Increasing concentrations of IL-3 and fusion proteins were added and the assay was carried out as described in Figure 2 and in Example 7. IL-3:Epo Flex (CHO CM containing IL-3:Epo fusion protein with a 23aa flexible linker); IL-3:Epo Short (CHO CM containing IL-3:Epo fusion protein with a 2aa linker); Epo:IL-3 Short (CHO CM containing Epo:IL-3 fusion protein with a 3aa linker).

Figure 4 shows FDC-P1/ER cells proliferate in response to the Epo moiety of the hybrid growth factors. FDC-P1/ER cells were grown to stationary phase and suspended in RPMI-1640 plus 10% FCS without growth factor for 16 hours. The indicated concentrations of growth factors were added for 42 hours followed by a 6 hour pulse of (³H) thymidine as described in Example 7. Columns are labeled as described in Figure 2. WEHI3 CM (medium conditioned by murine WEHI3 cells which produce and secrete IL-3).

Figure 5 shows dose response of FDC-P1/ER cells to the Epo moiety of the hybrid growth factors. FDC-P1/ER cells were grown to stationary phase and suspended in RPMI-1640 plus 10% FCS and deprived of growth factor for 16 hours. Increasing concentrations of Epo and fusion proteins were added and the assay was carried out as described in Example 7. Hybrid growth factors are as designated in Figure 3.

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Figure 6 shows IL-3 plus Epo responsiveness of IL-3 adapted TF-1 cells. TF-1 cells adapted for growth in IL-3 were grown to stationary phase and suspended in RPMI-1640 plus 10% FCS minus growth factor for 16 hours. Increasing concentrations of growth factors, 0.75 fmol/ml hybrid growth factors and 0.75 fmol/ml Epo plus 1.5 fmol/ml IL-3 (1), 1.5 fmol/ml hybrid growth factors and 1.5 fmol/ml of Epo plus 3.0 fmol/ml IL-3 (2), 3.0 fmol/ml hybrid growth factors and 3.0 fmol/ml Epo plus 6.0 fmol/ml IL-3 (3), were added and the assay was carried out as described in Example 7. Hybrid growth factors are as designated in Figure 3.

Figure 7 shows dose responsiveness of IL-3 adapted TF-1 cells to the hybrid growth factors. TF-1 cells adapted for growth in IL-3 were grown to log phase and suspended in RPMI-1640 plus 10% FCS minus growth factor for 16 hours. Increasing concentrations of hybrid growth factors were added and the cells were incubated for 8 hours. (³H) Thymidine (1 μ Ci/well) was added and the incubation was continued for 16 hours. (A) Dose response to hybrid growth factor, concentrations of 0 to 30 fmol/ml. (B) Represents the same data as in A for concentrations of 0 to 1.875 fmol/ml to emphasize the differences between hybrid factors. Hybrid growth factors are as designated in Figure 3.

Figure 8 shows dose responsiveness of GM-CSF adapted TF-1 cells to the hybrid growth factors. TF-1 cells maintained in GM-CSF were grown to log phase and suspended in RPMI-1640 plus 10% FCS minus growth factor for 16 hours. Increasing concentrations of hybrid growth factors were added and the assay was carried out as described above for Figure 5. (A) Dose response to hybrid growth factor concentrations, of 0 to 30 fmol/ml. (B) Represents the same data as in A for concentrations of 0 to 1.875 fmol/ml to emphasize the differences between hybrid factors. Hybrid growth factors are as designated in Figure 3.

Figure 9 shows TF-1 cells proliferate in response to the IL-3 moiety of the IL-3/G-CSF hybrid growth factor. TF-1 cells were grown to stationary phase and suspended in RPMI-1640 plus 10% FCS deprived of

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growth factor for 16 hours. The indicated concentrations of growth factors were added and the assay was carried out as described in Example 7. Factors are as designated in Figure 2 except, G-CSF (rHu G-CSF); IL-3/G-CSF (CHO CM containing IL-3/G-CSF fusion protein with a 10aa linker).

Figure 10 shows NFS-60 cells proliferate in response to the G-CSF moiety of the IL-3/G-CSF hybrid growth factor. NFS-60 cells were grown to stationary phase and suspended in RPMI-1640 plus 10% FCS minus growth factor for 16 hours. The indicated concentrations of growth factors were added and the assay was carried out as described in Example 7. Growth factors are as designated in Figures 2 and 9.

Figure 11 shows dose responsiveness of AML193 cells to the IL-3/G-CSF hybrid growth factor. AML193 cells were grown to stationary phase and suspended in RPMI-1640 plus 10% FCS deprived of growth factor for 16 hours. The indicated concentrations of growth factors were added and the assay was carried out as described in Example 7. Growth factors are as designated in Figures 2 and 9.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a recombinant hematopoietic molecule comprising at least a portion of a first hematopoietic molecule having early myeloid differentiation activity and at least a portion of a second hematopoietic molecule having late myeloid differentiation activity. This recombinant molecule has early myeloid differentiation activity associated with the first hematopoietic molecule and late myeloid differentiation activity associated with the second hematopoietic molecule. Within this application, "hematopoietic molecule" means a molecule which promotes and/or regulates hematopoiesis. Hematopoietic molecules exert such promotional or regulatory activities at different stages during hematopoiesis, such stages being referred to herein as early myeloid differentiation and late myeloid differentiation. Also within this application, "early myeloid differentiation activity" means the ability to promote the

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differentiation, self-renewal, or proliferation of pluripotent myeloid cells, i.e., stem cells or colony forming unit, granulocyte-erythrocyte-monocyte-megacaryocyte, cells. Moreover, within this application, "late myeloid differentiation activity" means
5 the ability to promote the maturation or differentiation of a lineage restricted myeloid cell, i.e., a myeloid precursor cell committed to a specific cell lineage such as erythrocytes, megakaryocytes, monocytes, neutrophils, eosinophils, and basophils.

10 In one embodiment of the invention, the first hematopoietic molecule is selected from the group consisting of IL-3 and GM-CSF. In another embodiment of the invention, the second hemopoietic molecule is selected from the group consisting of Epo, G-CSF, IL-5 and M-CSF. In
15 a preferred embodiment of the invention, the portion of the first hematopoietic molecule is linked to the portion of the second hematopoietic molecule by an amino acid linker sequence comprising at least two amino acid residues.

20 Within the context of the present invention, it is understood that variations in proteins and nucleic acids exist among individuals, e.g. amino acid or nucleotide substitutions, deletions, insertions, and degree or location of glycosylation, and that functional derivatives resulting therefrom are included within the scope of the present invention.

25 In a preferred embodiment of the invention, the recombinant molecule comprises the entire amino acid sequence of human IL-3 (SEQ ID NO: 1). Moreover, the recombinant hematopoietic molecule may preferably comprise a 79 amino acid sequence derived from human IL-3 (SEQ ID NO:
30 2), i.e. residues 1-79 of SEQ ID NO: 1.

Further still, in yet another preferred embodiment of the invention, the recombinant molecule comprises the entire amino acid sequence of human erythropoietin (SEQ ID NO: 3). In still a further embodiment of
35 the invention, the hemopoietic molecule comprises a 155 amino acid

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sequence derived from human erythropoietin (SEQ ID NO: 4), i.e., residues 7-161 of SEQ ID NO: 3.

5 In another preferred embodiment of the invention, the recombinant hematopoietic molecule comprises the entire amino acid sequence of human G-CSF (SEQ ID NO: 5).

10 In one embodiment of the invention, the first hematopoietic molecule is IL-3 and the second hematopoietic molecule is erythropoietin. The first hematopoietic molecule, i.e. IL-3, may comprise the amino portion and the second hematopoietic molecule, i.e. Epo, may comprise the carboxyl portion of the recombinant molecule. Preferably, the recombinant hematopoietic molecule comprises the amino acid sequence from amino acid 1 to amino acid 302 of SEQ ID NO: 6. Also preferably,
15 the recombinant hematopoietic molecule comprises the amino acid sequence from amino acid 1 to amino acid 321 of SEQ ID NO: 7. However, in another embodiment of the invention, the first hematopoietic molecule, i.e. IL-3, may comprise the carboxyl portion and the second hemopoietic molecule, i.e. Epo, may comprise the amino
20 portion of the recombinant molecule. In a preferred embodiment of the invention, the recombinant molecule comprises the amino acid sequence from amino acid 1 to amino acid 303 of SEQ ID NO: 8. In yet another preferred embodiment, the recombinant molecule comprises the amino acid sequence from amino acid 1 to amino acid 322 of SEQ ID NO: 9.

25 In still a further embodiment of the invention, the first hematopoietic molecule is IL-3 and the second hematopoietic molecule is G-CSF. In one such embodiment, the first hematopoietic molecule comprises the amino portion and the second hematopoietic molecule
30 comprises the carboxyl portion of the recombinant molecule. In yet a more specific embodiment, the recombinant molecule comprises the amino acid sequence from amino acid 1 to amino acid 317 of SEQ ID NO: 10.

35 The subject invention also provides nucleic acid molecules which encode the recombinant hematopoietic molecules of the subject invention. Examples of such nucleic acid molecules are SEQ ID NO: 11,

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SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14 and SEQ ID NO: 15. Moreover, vectors which comprise the nucleic acid molecules of the subject invention are also disclosed. In one embodiment of the invention, the vector comprises a plasmid. Moreover, host vector
5 systems for the production of a recombinant hematopoietic molecule of the present invention are provided which comprise a vector of the present invention in a suitable host, preferably a mammalian cell such as a CHO or COS cell. This host vector system may be grown under suitable conditions which permit the expression of the recombinant
10 hematopoietic molecule, which may be recovered by purification techniques known in the art, e.g. ion exchange chromatography, affinity chromatography, and size exclusion chromatography.

The present invention further provides pharmaceutical compositions
15 useful for treating patients suffering from anemias of various origins, e.g. renal failure, and AIDS. Moreover, these pharmaceutical compositions are useful for administering to patients for preoperative autologous blood donations, patients receiving or donating bone marrow for transplantation purposes, and patients undergoing cancer
20 chemotherapy. These pharmaceutical compositions comprise effective hematopoiesis-promoting amounts of a recombinant molecule of the present invention and a pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers are known in the art and are disclosed in The Pharmacopeia of the United States and the National
25 Formulary. Depending on the specific application contemplated, the pharmaceutical composition may be formulated as a solution, suspension, parenteral preparation, or spray. Parenteral preparations may include a vehicle such as specially distilled, pyrogen-free water, phosphate buffer, or normal saline. Oral and/or transmucosal dosage
30 forms may comprise phospholipids, often in the form of liposomes.

Also provided is a method for treating a patient to promote hematopoiesis which comprises administering to the patient an
35 effective hematopoiesis-promoting amount of a pharmaceutical composition of the present invention.

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The recombinant hematopoietic molecules, nucleic acid molecules, pharmaceutical compositions and methods of the present invention will be better understood by reference to the following experiments and examples, which are provided for purposes of illustration and are not
5 to be construed as in any way limiting the scope of the invention, which is defined by the claims appended hereto.

Examples

10 Construction of the hybrid protein genes: Genes encoding IL-3 (SEQ ID NO: 16), Epo (SEQ ID NO: 17) and G-CSF (SEQ ID NO: 18) were purchased from British Biotech. Ltd. These genes were utilized to construct three different hybrid hematopoietic proteins, i.e., IL-3:Epo,
15 Epo:IL-3 and IL-3:G-CSF. In these hybrids the first named gene forms the amino portion and the second named gene the carboxyl portion of the hybrid protein.

Example 1

20 A nucleic acid molecule encoding an IL-3:Epo hybrid growth factor was constructed as follows: CSF, the native leader sequence of IL-3 was synthesized as 4 oligonucleotides (SEQ ID NOS: 19-22; see Table I) which represents both strands of the leader sequence. In addition, the 5' end of the leader (SEQ ID NO: 19) encoded a convenient
25 restriction enzyme overhang (EcoRI), although the EcoRI site was not regenerated, in front of the ATG start codon. The 3' end of the leader (SEQ ID NO: 21) included the first several amino acid codons of IL-3 and an SpeI overhang so that the annealed leader sequence could be easily ligated to IL-3, which was altered by British Biotech to
30 include an SpeI site. The leader sequence was annealed and ligated to pKS (Stratagene Cloning Systems, Inc., San Diego, CA) cleaved with EcoRI and SpeI. The resulting plasmid was designated pKS0. The IL-3 containing pUC18 plasmid obtained from British Biotech was cleaved with SpeI and NheI, then ligated to a linker oligonucleotide
35 (complimentary oligonucleotide SEQ ID NOS: 23 and 24; see Table I) which contained the following three restriction sites: NheI, XbaI and

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NcoI. Cleavage was then performed with SpeI and XbaI. The resulting 379 base pair fragment was then ligated to PKSO cleaved with

5 SpeI and XbaI. The resulting plasmid (pKSOIL-a) contained the IL-3 leader, the IL-3 gene and a small linker fragment.

10 The Epo gene was inserted into pEe6 (Celltech, Ltd., Slough, U.K.), a mammalian expression vector which contains the human Cytomegalovirus promoter, a polylinker region and a poly-A addition site in addition to ampicillin resistance and a bacterial origin of replication, by
15 cleaving the Epo containing plasmid obtained from British Biotech with HindIII and BamHI. Epo was then cleaved with NcoI. The same linker comprising oligonucleotide SEQ ID NOS: 23 and 24 as described earlier was ligated to Epo and then cleaved with XbaI to yield the entire Epo
20 gene. This was then ligated to XbaI and BclI cleaved pEe6 to yield pEe6 containing the Epo gene (pEepo). PKSOIL-a was cleaved with EcoRV and an XbaI linker was ligated to the blunt ends followed by cleavage with XbaI, which released the IL-3 gene with the leader sequence. This was then ligated to XbaI cleaved pEepo to yield a plasmid
25 containing an entire hybrid protein gene (pEepie-a) (see SEQ ID NO: 11 for the structure of the inserted hybrid gene, designated herein IL-3:Epo Short). The glutamine synthetase (gs) gene was then inserted into the BamHI site of pEepie-a to yield pEepogs-a or pEepogs-b, depending upon the orientation of the gs gene. Glutamine synthetase
30 confers resistance to methionine sulfoximine (MSX) in order to select cells which have taken up the plasmid after transfection. After the plasmid was constructed a large batch was grown, purified by CsCl ultracentrifugation, and used for transfection. At each step in this process all ligation joints between fragments were analyzed by DNA
35 sequence analysis in order to assure that there were no changes that would cause frameshifts and prevent the hybrid gene from being expressed.

To construct a nucleic acid molecule encoding an IL-3:Epo hybrid growth factor with a longer linker sequence separating IL-3 and Epo, pEepie-a was cleaved with NheI and annealed oligonucleotide SEQ ID

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NOS: 25 and 26 (see Table I) were ligated into the cleaved plasmid. This linker encodes the flexible amino acid sequence Gly Ser Gly Ser Gly Ser (SEQ ID NO: 27). Clones with the insert in the proper orientation were selected by probing colonies with the junction
5 oligonucleotide SEQ ID NO: 28 (see SEQ ID NO: 14 for the structure of the inserted hybrid gene, designated herein IL-3:Epo Flex). The glutamine synthetase gene was then added to the construct as described above.

10 Example 2

A nucleic acid molecule encoding an IL-3:G-CSF hybrid growth factor was constructed as follows: pUC18 containing G-CSF (British Biotech) was cleaved with HindIII. A linker composed of an overhanging XbaI
15 site, a NotI site and an overhanging HindIII site (oligonucleotide SEQ ID NOS: 29 and 30; see Table I) was ligated to the pUC18:G-CSF. This was then cleaved with XbaI and BamHI which released the entire G-CSF gene. The G-CSF fragment was then inserted into XbaI and BclI cleaved pEe6 (pEe6:G-CSF). IL-3 with its signal sequence was removed from
20 the IL-3:Epo plasmid pEepogs-a as an XbaI fragment. This IL-3 fragment was then inserted into XbaI cleaved pEe6-G-CSF. After restriction analysis, a plasmid containing the IL-3 gene in the proper orientation was obtained (pEG11), this plasmid encoded a gene capable of expressing IL-3 and G-CSF as a hybrid protein (see SEQ ID NO: 13
25 for the structure of the inserted hybrid gene, designated herein IL-3:G-CSF). The gs gene was inserted into this plasmid as described in Example 1 above to yield plasmids pEG13 and pEG14, depending upon the orientation of the gs gene.

30 Example 3

A nucleic acid molecule encoding an Epo:IL-3 hybrid growth factor was constructed by first synthesizing the native Epo signal sequence as
35 oligonucleotide SEQ ID NOS: 31-36 (see Table I). These were annealed to yield an overhanging 5' XhoI sequence and a 3' PstI sequence. These were then ligated and subcloned as an XhoI/PstI fragment

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(pEpo1). In order to obtain the proper reading frame and signal sequence processing site, the plasmid containing the signal sequence was cleaved with PstI and the 3' overhang left by PstI was enzymatically removed with T4 polymerase. This was then cleaved with BamHI. The Epo gene was then amplified by PCR as a fragment with a 5' blunt end using oligonucleotide SEQ ID NO: 37 as a primer and a 3' BamHI end using oligonucleotide SEQ ID NO: 38 as a primer. This fragment was then ligated into pEpo1 to yield a complete Epo gene with its leader sequence. PCR was used to amplify the Epo gene with its signal sequence as an (5') XbaI and (3') NotI fragment using oligonucleotide SEQ ID NOS: 39 and 40 as primers. This was then digested with XbaI and NotI. At the same time, a purified IL-3 fragment was amplified by PCR as a (5') NotI and (3') BamHI fragment using oligonucleotide SEQ ID NOS: 41 and 42, followed by digestion with NotI and BamHI. These two fragments were ligated to pEe6 cleaved with XbaI and BclI to yield a full length hybrid gene encoding both Epo and IL-3 (pEG16) (see SEQ ID NO: 12 for the structure of the inserted hybrid gene, designated herein Epo:IL-3 Short). The gs gene was inserted as described in Example 1 above to yield pEG17 and pEG18, depending upon the orientation of the gs gene.

A flexible linker is inserted into Epo:IL-3 by cleaving pEG17 or pEG18 with NotI. Annealed oligonucleotide SEQ ID NOS: 43 and 44 are then ligated into the cleaved plasmid. Clones with the insert in the proper orientation are selected by probing colonies with a junction oligonucleotide as described above (see SEQ ID NO: 15 for the structure of the inserted hybrid gene.)

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TABLE I
OLIGONUCLEOTIDES

All oligonucleotides are listed in the 5' to 3' orientation:

- 5 AATTGCCGCC ACCATGAGCC GCCTGCCCCT CCGTCTCT (SEQ ID NO: 19)
GCTCCAATC CTGGTCCGCC CCGGACTCCA AGCTCCCATG ACCCAGACAA (SEQ ID NO: 20)
CTAGTTGTCT GGGTCATGGG AGCTTGGAGT CCGGGGCGG (SEQ ID NO: 21)
ACCAGGAGTT GGAGCAGGAG CAGGACGGGC AGGCGGCTCAT GGTGGCGGC (SEQ ID NO: 22)
CTAGCGATCT TTCTAGA (SEQ ID NO: 23)
- 10 CATGTCTAGA AAGATCG (SEQ ID NO: 24)
CTAGAAGCGG CCGCA (SEQ ID NO: 29)
TTCGCCGGCG TTCGA (SEQ ID NO: 30)
TCGAGCCATG GGGGTGCACG AATGTCCT (SEQ ID NO: 31)
GCCTGGCTGT GGCTTCTCCT GTCCCTGCTG TC (SEQ ID NO: 32)
- 15 GCTCCCTCTG GGCTCCCAG TCCTGGGCTG CA (SEQ ID NO: 33)
GCCCAGGACT GGGAGGCCCA GAGGGA (SEQ ID NO: 34)
GCGACAGCAG GGACAGGAGA AGCCACAGCC AGGCAGGACA TT (SEQ ID NO: 35)
CGTGACCCCC CATGGC (SEQ ID NO: 36)
GCCCCACCAC GCCTCATCTG T (SEQ ID NO: 37)
- 20 GAATTCGGAT CCTTATCATC T (SEQ ID NO: 38)
CTAGTCTCTA GAATGGGGGT CCACGAATGT (SEQ ID NO: 39)
AGCCATGGCG GCCGCTCTGT CCCCTGTCCT (SEQ ID NO: 40)
GACAGAGCGG CCGCCATGGC TCCCATGACC (SEQ ID NO: 41)
GAATTCGGAT CCTTACTAAA AGATCGCTAG (SEQ ID NO: 42)
- 25 CTAGCGTCCG GAGGCGGTGG CTCGGGCGGT GCGGCTCGG GTGGCGGC GCTCTGCG
(SEQ ID NO: 25)
CTAGCGCAGA GCCGCCGCCA CCGCAGCCGC CACCGCCCGA GCCACCGCC TCCGGACG
(SEQ ID NO: 26)
TTGTCGCTAG CGTCCGGAGG C (SEQ ID NO: 28)
- 30 GGCCGCTTCC GGAGGCGGTG GTCGGGCGG TGGCGGCTCG GGTGGCGGC GGCTCTGC
(SEQ ID NO: 43)
GGCCGCAGAG CCGCGCCAC CCGAGCCGCC ACCGCCGAG CCACCGCCT CCGGCAGC
(SEQ ID NO: 44)

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Example 4

Transfection of the hybrid gene containing plasmids. All transfections were performed using the Lipofecting transfection kit (Bethesda Research Labs, Gaithersburg, MD) using 15-30 mg. of purified plasmid DNA (pEepogs-a, pEepogs-b, pEG13, pEG14, pEG17, and pEG18). The following alterations were made to the protocol provided by the company: the growth medium in these experiments was GMEM-S and the CHO-K1 cells were incubated in the presence of 10% CO₂; after addition of the lipofectin:DNA complex, cells were incubated without selection for 24 hours. The cells were transferred to GMEM-S supplemented with 25 mM MSX after 24 hours. The MSX concentration was subsequently increased to 50 mM after one week. Cloning rings were used to subclone MSX resistant colonies and each of these colonies was placed into an individual well of a 24 well plate. Selected clones were incubated in the absence of MSX to insure that the hybrid protein gene was stably integrated. Strongly positive clones were grown in large cultures to provide larger amounts of hybrid proteins for further analysis.

20

Example 5

Assays for hybrid protein production. Cell supernatants from transfected or control cells were assayed using several different assays. In order to demonstrate Epo production, an RIA kit for Epo was used (Incstar Corp., Stillwater, MN). The presence of IL-3 was determined using an ELISA assay in which the capture antibody was a polyclonal goat anti-IL-3 (R&D Systems, Minneapolis, MN) and the probe antibody was a murine anti-IL-3 monoclonal. Goat anti-mouse conjugated to horseradish peroxidase followed by suitable substrate was used to detect the presence of the monoclonal anti-IL-3. A very similar assay was used to demonstrate the presence of the hybrid proteins except that a murine anti-Epo monoclonal or anti-G-CSF monoclonal was used in place of anti-IL-3 monoclonal. Additionally, IL-3:Epo Short was analyzed by Western blot analysis. The blot was probed with antibody to Epo and then with ¹²⁵I goat anti-mouse. A

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single broad band appeared on the autoradiogram with a molecular weight of slightly more than 50,000 daltons.

Example 6

5

Cellular assays. Epo and/or IL-3 dependent and responsive cell lines were used to test the biological activities of the hybrid proteins. B6SutA (5) is a multipotential hematopoietic progenitor cell line established from nonadherent cell populations removed from continuous B6.S mouse bone marrow culture. This cell line demonstrates absolute dependence upon a source of growth factor(s). In response to Epo a population of the cells synthesize hemoglobin. Studies of globin expression indicated that the globin programs of B6SutA cells are similar to those of erythroid progenitors at the period of transition from the yolk sac to fetal liver erythropoiesis. TF-1 (6) it is a cell line of immature erythroid origin established from a patient with erythroleukemia. The cell line shows complete dependency on GM-CSF or IL-3. Epo sustains short-term growth of TF-1 and will induce hemoglobin synthesis in a very small population of cells (8%). Hemin and w-aminolevulinic acid induce hemoglobin synthesis in most of the cells.

Human IL-3 will not bind the murine IL-3 receptor, therefore experiments that were done with B6SutA cells measured only the functionality of the Epo moiety of the hybrid. B6SutA cells are carried in murine IL-3. In each experiment, they are washed thoroughly and set up with growth factors at 10^5 cells/ml. Cell growth and hemoglobin content were monitored on days 3 and 6 of each experiment. Cells grown in the presence of concentrated (10X) CHO conditioned medium (CM) containing IL-3:Epo Short at a final concentration equivalent to 4.8 units/ml of Epo grew as well as cells grown in an equivalent amount of recombinant human (rHu) Epo. The percentage of cells which synthesized hemoglobin in response to the CHO-IL-3:Epo Short CM was always four times that of cells exposed to rHu Epo. B6SutA cells grown in the presence of rHu IL-3 and rHu Epo grew as well as cells grown in the presence of IL-3:Epo Short and

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induced hemoglobin synthesis in the same percentage of cells as did rHu Epo. Cells exposed to recombinant murine IL-3 (rMu IL-3) and rHu Epo grew similarly to cells exposed to rMu IL-3 alone and neither effectively induced cells to synthesize hemoglobin. Concentrated
5 control CHO CM did not support the growth of B6SutA cells nor did it induce hemoglobin synthesis. CHO CM plus rHu Epo supported cell growth and hemoglobinization as well as CHO-IL-3:Epo Short CM.

CHO-IL-3:Epo Short CM as well as CHO-rHu IL-3 CM both supported growth
10 of human TF-1 cells. Control CHO CM supported only limited growth of the TF-1 cells.

Discussion

15 The above-mentioned results demonstrate that a hybrid protein comprising two growth factors can be expressed in mammalian cell culture systems. In vitro assays of IL-3:Epo Short indicate that this hybrid protein has the activities of both IL-3 and Epo. The therapeutic application of such hybrid factors has advantages over
20 using two factors separately simply in terms of patient administration, and moreover since the production, purification and formulation of one factor is less labor intensive than for two separate factors.

25 **Example 7**

Factor Dependent Cell Lines and Culture Media - The GM-CSF/IL-3/Epo dependent human TF-1 cell line and the G-CSF dependent murine NFS-60 cell line were grown and maintained as described (7,8,). The GM-CSF
30 dependent human cell line AML 193 (9) was adapted for growth in IL-3 by continuous culture of the cells in RPMI-1640 plus 10% FCS supplemented with rHu IL-3 for 6 weeks. The TF-1 derived cell line, TF-136 was selected by continuous culture of the TF-1 line in RPMI-1640 plus 10% FCS supplemented with 5ng/ml of rHu IL-3 for 6
35 months, followed by single cell suspension cloning of the resultant IL-3 dependent cells. The Epo dependent murine cell line, FDC-P1/ER,

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was derived from the IL-3 dependent line, FDC-P1, by introduction of the murine Epo receptor into these cells. (10) FDC-P1/ER cells are maintained in RPMI-1640 plus 10% FCS supplemented with 1 unit/ml of rHu Epo. Recombinant human Epo was obtained from Ortho Biologicals, Inc (Raritan, NJ). Recombinant human IL-3, rHu G-CSF and rHu GM-CSF were purchased from R & D Systems (Minneapolis, MN).

Capture ELISA Assay - ELISA plate was coated with 5 µg/200 µl/well of goat anti-human IL-3 (R & D Systems) in PBS at 40°C overnight. Excess antibody was removed by washing with PBS. Blocking was carried out with 300 µl/well of 1% non-fat milk in PBS for 1 hour at 37°C followed by washing with 0.05% Tween™ in PBS. Samples were then incubated with the IL-3 antibody for 1 hour at 37°C in 0.5% non-fat milk, 0.025% Tween™. Following extensive washing, the second antibody, a mouse anti-Epo monoclonal (Genzyme, Cambridge, MA), was added to the plate which was incubated for 1 hour at 37°C. The plate was washed and incubated with conjugate antibody (Goat anti-mouse-horseradish peroxidase) for 30 minutes at 37°C. Color development was carried out with the addition of o-phenylenediamine/H₂O₂ at room temperature (RT) for 30 minutes. The reaction was stopped with 1N H₂SO₄ and the samples were read at 495 nm.

Gene Amplification- CHO cell lines producing significant amounts of the hybrid growth factors were isolated and 10⁶ cells were plated in a 75 mm T-flask in GMEM-S medium containing various concentrations of methionine sulphoximine (MSX), ranging between 100µM and 500µM. Colonies resistant to the highest MSX concentration (IL-3:Epo Flex 200µM; IL-3:Epo Short 250µM; Epo:IL-3 Short 250µM; IL-3:G-CSF 250µM) were isolated and expanded. Those clones producing the highest levels of hybrid growth factors as determined by Epo or G-CSF ELISA assay (Amgen) were used for subsequent studies. IL-3:Epo Flex (clone 23-10); IL-3:Epo Short (clone 5-4); Epo:IL-3 Short (17-3-1).

Cell Proliferation Assays - Factor dependent cells were grown to stationary phase, washed, and incubated for 16 hours in media plus 10% FCS deprived of growth factor. The cells were plated at a

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- concentration of 2×10^5 cells/ml in a 96 well microtiter plate (200 μ l/well) with and without growth factor. Recombinant human growth factors were diluted into CHO conditioned medium (CM) before addition to cells. Following incubation for 42 hours, (3 H) thymidine (1 μ Ci/well; New England Nuclear, Boston, MA) was added and the cells were incubated for another 6 hours. The cells were then hypotonically lysed and harvested onto glass fiber filters. The filters were washed with distilled water, dried and counted in liquid scintillation fluid.
- 5
- 10 Bone Marrow Cultures - Informed consent was obtained prior to aspirating bone marrow from normal volunteers. Aspirated bone marrow was diluted 1:1 in α - medium without nucleosides containing preservative-free sodium heparin. A single cell suspension was prepared, layered, over an equal volume of Ficoll-Hypaque (sp gr 1.077
- 15 g/ml) and then centrifuged for 25 minutes at 1,500 rpm at 40°C. The light-density mononuclear cells were collected and washed and diluted to 5×10^5 cells/ml with Iscove's modified Dulbecco's medium plus 20% modified FCS (Gibco BRL). Cells (1.25×10^5 /ml) were plated in 0.8% methylcellulose supplemented with various concentrations of rHu Epo,
- 20 rHu IL-3 and hybrid growth factors. Cultures were incubated for either 7 or 14 days in a humidified atmosphere with 5% CO₂ at 37°C. Colonies were counted at day 7 for CFU-E and at day 14 for BFU-E under an inverted microscope.
- 25 Western Blot Analysis - CHO CM containing approximately 75 ng of IL-3:Epo fusion protein was electrophoresed on a 10-20% gradient SDS PAGE gel (Integrated Separations Systems) under reducing and denaturing conditions. Samples were loaded in 0.0625 M Tris-HCl (pH 6.8), 2% SDS, 5% 2-mercaptoethanol, 10% glycerol and 0.002% bromophenolblue
- 30 following heat treatment at 100°C for 3 minutes. The proteins were transferred to nitrocellulose (Bio Rad) in 25 mM Tris, 129 mM glycine, pH 8.3, 20% methanol, at 150 V, constant power, for 90 minutes. The transfer efficiency was monitored by visual examination of the completeness of transfer of prestained molecular weight markers (Bio
- 35 Rad). The nitrocellulose membrane was incubated in PBS containing 3% BSA for 1 hour at room temperature and subsequently washed in PBS

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containing 0.5% Tween (PBS-T) for 5 minutes at room temperature. The membrane was probed with primary anti-Epo anti-sera in 3% BSA in PBS. Excess antibody was removed by 3, 5 minute room temperature washes in PBS-T. The nitrocellulose membrane was then probed with a secondary antibody conjugate (Goat anti-Rabbit IgG/ Alkaline Phosphatase, Bio Rad) for 1 hour at room temperature. Excess secondary antibody was removed by two washes with PBS-T as above. Color development was carried out by incubation with color reagents (Bio Rad) in alkaline phosphatase buffer (100 mM Tris HCl, pH 9.5, 100 mM NaCl, 5 mM MgCl₂). The reaction was stopped by immersion of the membrane in cold (4°C) distilled H₂O.

Results and Discussion

Hybrid growth factor plasmid amplification. Individual transfected CHO cell clones producing significant amounts of the desired hybrid growth factor were identified by ELISA capture assay, Table II. The clones were plated out and placed in medium with increasing concentrations of MSX, ranging between 100 μ M and 500 μ M. Colonies surviving at the highest concentration of MSX were isolated and grown to confluence. Serum and drug-free medium was then added to the cells and collected after 4 days. At the time of collection fresh serum and drug-free medium was added to the cells. A total of 3 collections were taken. The amount of hybrid growth factor produced in the collections was determined by Epo or G-CSF ELISA assay (Table III) and appropriate collections were pooled. The pooled CM was used as a source of hybrid growth factors in all cellular assays.

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TABLE II

	<u>Hybrid Growth Factor</u>	<u>OD (495 nm)</u>
	CHO CM*	0.24
	IL-3:Epo Flex	2.44
5	IL-3:Epo Short	2.46
	Epo:IL-3 Short	1.59
	IL-3:G-CSF	2.40
10	* Conditioned medium from CHO cells transfected with the vector pEe6.	

TABLE III

	<u>Hybrid Growth Factor</u>	<u>Collection</u>	<u>Concentration (μg/ml)*</u>
	IL-3:Epo Flex	1st	3.0
15		2nd	4.2
		3rd	3.3
	IL-3:Epo Short	1st	1.5
		2nd	5.8
		3rd	6.7
20	Epo:IL-3 Short	1st	26.7
		2nd	53.3
		3rd	58.7
	IL-3:G-CSF	1st	2.2
		2nd	2.0
25		3rd	2.0

* Concentrations were determined by Epo and G-CSF ELISA Assay.

Detection of hybrid growth factor production. In order to confirm that the IL-3 and Epo detected in the ELISA capture assays were being produced in the form of a fusion protein, Western blot analysis was performed. Conditioned medium from CHO cells transfected with IL-3:Epo Flex cDNA (Figure 1, lane 2), IL-3:Epo Short cDNA (Figure 1, lane 3) and Epo:IL-3 Short cDNA (Figure 1, lane 4) were probed with mouse anti-Epo polyclonal anti-sera. Immunoreactive material corresponding to a molecular weight of approximately 50,000 daltons,

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the expected size of the IL-3:Epo and Epo:IL-3 hybrid growth factors, was detected in each sample. Comparison with increasing concentrations of rHu Epo (Figure 1, lanes 6-10) indicated that the antibody used in this analysis recognizes the Epo moiety of the fusion proteins efficiently.

IL-3 bioactivity of the IL-3:Epo and Epo:IL-3 hybrid growth factors.

To determine whether the IL-3 moiety of the IL-3:Epo and Epo:IL-3 hybrid growth factors was functional, its ability to support growth of the IL-3-dependent human cell line, AML193, was evaluated (Figure 2).

As Epo does not support growth of these cells (Figure 2), only IL-3 activity was measured in this assay system. CHO CM containing rHu IL-3 and levels of hybrid growth factors sufficient to support maximal proliferation were added to the culture medium. The cells were then pulsed with (^3H) thymidine and the radioactivity incorporated into the DNA was used as a measure of cell growth. Cells exposed to CHO CM containing no growth factors, supported the proliferation of AML193 cells to the same extent as did cells grown in medium alone. Each of the fusion proteins when present in excess, supported the growth of AML193 cells in a manner equivalent to that of rHu IL-3.

The functional activity of the IL-3 portion of the IL-3:Epo and Epo:IL-3 hybrid growth factors was further evaluated by comparing the fusion proteins to rHu IL-3 in dose response experiments (Figure 3). The incorporation of (^3H) thymidine into AML193 DNA was again used as a measure of cell proliferation. When IL-3 was located at the N-terminus of the hybrid growth factor protein (IL-3:Epo), its ability to support AML193 proliferation was equivalent to that of rHu IL-3 ($\text{ED}_{50} = 5 \text{ fmol/ml}$). Size (2 aa versus 23 aa) and flexibility of the linker did not greatly impact the function of the IL-3 moiety. However, when IL-3 was located at the C-terminus of the fusion protein (Epo:IL-3), its ability to support the growth of AML193 cells was less ($\text{ED}_{50} = 200 \text{ fmol/ml}$) than that of rHu IL-3 and the IL-3:Epo hybrid factors. These results suggest that linkage of IL-3 at the N-terminus interferes with function while linkage at the C-terminus does not. It has previously been reported that modification of the C-terminus of

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murine IL-3 did not interfere with its activity (11). Therefore, it should be possible to target any molecule or compound of interest to cells expressing the IL-3 receptor through linkage to IL-3 at its C-terminus.

5

Epo bioactivity of the IL-3:Epo and Epo:IL-3 hybrid growth factors.

To determine whether the Epo moiety of the hybrid growth factors was functional, its ability to support the growth of the Epo-dependent murine cell line FDC-P1/ER, was evaluated (Figure 4). This line
10 derived from FDC-P1 cells expresses the murine Epo receptor (10), and is dependent on either murine IL-3 or Epo (murine and human) for growth (Figure 4). As IL-3 is a species specific growth factor, murine IL-3-dependent cells do not respond to human IL-3 (12). Therefore, when using the FDC-P1/ER cell line to evaluate
15 functionality, only the activity of the Epo moiety is measured. CHO CM containing rHu Epo and levels of hybrid growth factors sufficient to support maximal proliferation were added to the culture medium. The cells were then pulsed with (^3H) thymidine and the radioactivity incorporated into the DNA was used as a measure of cell growth. Cells
20 exposed to CHO CM which did not contain cytokines did not support the proliferation of FDC-P1/ER cells. Each of the fusion proteins when present in excess, stimulated the growth of FDC-P1/ER cells to the same extent as did rHu Epo. (Figure 4)

25 The biological function of the Epo portion of the IL-3:Epo and Epo:IL-3 hybrid growth factors was further analyzed by comparing the fusion proteins to rHu Epo in dose response experiments (Figure 5). The incorporation of (^3H) thymidine into FDC-P1/ER cells was used as a measure of cell proliferation. Each of the hybrid growth factors was
30 equivalent to rHu Epo in ability to stimulate proliferation of FDC-P1/ER cells ($\text{ED}_{50} = 50 \text{ fmol/ml}$). Size (2-3 aa versus 23 aa) and flexibility of the linker, as well as the orientation of Epo within the protein (N-terminus versus C-terminus) did not alter function. Evidence exists suggesting that the N-terminus of Epo is not involved
35 in receptor binding as a monoclonal antibody directed toward the N-terminus of Epo does not neutralize its activity (13). The results

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presented here suggest that linkage of Epo to a second protein does not impair its ability to bind its receptor or transduce a signal. Epo could therefore be useful as a carrier protein which would target a molecule or compound of interest to those cells expressing the Epo receptor.

IL-3 plus Epo bioactivity of the IL-3:Epo and Epo:IL-3 hybrid growth factors. In order to study the effects of IL-3 and Epo in combination, proliferation of a human cell line, TF-1 (7), dependent on IL-3 and Epo for growth was measured. This experiment was done on a cytokine weight basis and the results are represented on a molar basis (Figure 6). rHu IL-3 (R & D Systems) made in E. coli is nonglycosylated. rHu Epo and hybrid growth factors made in CHO cells are glycosylated. Therefore, when equal weights of the growth factors were added to the cell culture medium, approximately twice the number of unglycosylated molecules of IL-3 were added as compared to glycosylated Epo and hybrid growth factor molecules.

CHO CM containing rhu IL-3 plus rHu Epo and levels of hybrid growth factors which support suboptimal proliferation of TF-1 cells adapted for growth in IL-3 were added to the culture medium. Cell growth was monitored by radioactivity incorporated into the DNA. (Figure 6) The activities of IL-3 plus Epo were not synergistic in this cell line, nor were they additive. At these low levels, the activities of the IL-3:Epo Flex and IL-3:Epo Short fusion proteins were comparable to those of a mixture of the two cytokines. Epo:IL-3 Short activity was again reduced in comparison to that of the IL-3:Epo hybrid growth factors and the combination of IL-3 plus Epo. This is likely to be due to decreased IL-3 activity.

The biological activity of the IL-3:Epo and Epo:IL-3 hybrid growth factors was further evaluated in dose response experiments (Figures 7 & 8). TF-1 cells adapted for optimal growth in IL-3 were exposed to CHO CM containing hybrid growth factors (Figure 7). Each of the fusion proteins when present in excess were able to support growth of the cells to the same extent (Figure 7A). At lower doses, the IL-

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3:Epo Flex protein appeared to be slightly more potent than the short
linkered hybrids (IL-3:Epo Flex ED50 = 0.37 fmol/ml; IL-3:Epo Short
ED50 = 0.75 fmol/ml; Epo:IL-3 Short ED50 = 0.9 fmol/ml) (Figure 7B).
This result was more pronounced in experiments done with TF-1 cells
5 adapted for optimal growth in GM-CSF (Figure 8). The IL-3:Epo Flex
protein was dramatically more potent than the hybrid growth factors
containing short linkers (IL-3:Epo Flex ED50 = 0.07 fmol/ml; IL-3:Epo
Short and Epo:IL-3 Short ED50 = 0.75 fmol/ml (Figure 8B). When
present in excess with the GM-CSF adapted TF-1 cells, each of the
10 fusion proteins stimulated cell proliferation to a similar extent
(Figure 8A). These results suggest that when IL-3 and Epo are fused,
the 23 aa flexible linker allows more efficient receptor interaction
than does a short (2-3 aa) linker.

15 It appears that induction of receptor expression is possible by
growing a cell in the presence of a cytokine whose receptor it has the
potential to express. An up regulation of Epo receptor expression has
been reported in IL-3-dependent cells transferred into medium
supplemented with Epo (14). Thus, it is likely that growing TF-1
20 cells in IL-3 or GM-CSF, preferentially increases the appearance of
cell surface IL-3 or GM-CSF receptors. Several research groups
(15-20) have observed a subset population of GM-CSF and IL-3 receptors
on primary human cells and hematopoietic cell lines capable of binding
both GM-CSF and IL-3. It has been suggested that a single accessory
25 molecule preferentially interacts with this subset of GM-CSF/IL-3
receptors allowing the transduction of signal. Our results raise the
possibility that GM-CSF could be inducing the expression of an
accessory molecule in TF-1 cells which may be important for binding
and could possibly link IL-3:Epo signal transduction. This protein
30 could be identical to the GM-CSF/IL-3 receptor accessory protein.

Erythroid colony formation stimulated by IL-3:Epo and Epo:IL-3 hybrid
growth factors. To assess the biological activity of the fusion
proteins on normal hematopoietic progenitor cells, analysis of the
35 formation of erythroid (BFU-E and CFU-E) colonies from nonadherent
mononuclear human bone marrow cells was performed. (Table IV) As was

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observed with the cell lines, the Epo moiety of each of the fusion proteins was equally active (CFU-E formation) on bone marrow progenitor cells. The IL-3:Epo Flex protein was the most active hybrid growth factor while the Epo:IL-3 Short protein was the least. (It stimulated two-thirds the number of BFU-E as did the IL-3:Epo Flex.) These results suggest that the IL-3:Epo Flex fusion protein may have significant clinical benefits where indications for combination therapy with IL-3 and Epo may prove efficacious.

10

TABLE IV

Growth Factors	BFU-E ^{a,b}	CFU-E ^c
No Factors	-	-
0.2 pmol/ml IL-3	-	-
15 0.1 pmol/ml Epo	+	+++
0.2 pmol/ml IL-3 &		
0.1 pmol/ml Epo	+++	+++
0.1 pmol/ml IL-3:Epo Flex	+++	+++
0.1 pmol/ml IL-3:Epo Short	++	+++
20 0.1 pmol/ml Epo:IL-3 Short	+	+++

a Mononuclear human bone marrow cells were used as a target cell population.

b BFU-E were counted 14 days after plating.

25 c CFU-E were counted 7 days after plating.

IL-3 bioactivity of the IL-3:G-CSF hybrid growth factor. To determine whether the IL-3 moiety of the IL-3:G-CSF hybrid growth factor was functional, its ability to support growth of the IL-3-dependent human cell line TF-1, was evaluated in a dose response experiment (Figure 9). Quantitation of IL-3:G-CSF protein in CHO CM was performed using a G-CSF ELISA assay in which the standard is unglycosylated G-CSF. Since the IL-3:G-CSF fusion protein is glycosylated, measurements are approximate. G-CSF does not support growth of TF-1 cells (Figure 9), therefore, the only activity measured in this assay system was IL-3.

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CHO CM containing rhu IL-3, rHu G-CSF, and IL-3:G-CSF hybrid growth factor were added to the culture medium. The radioactivity incorporated into the DNA was used as a measure of cell proliferation. CHO CM did not support growth of TF-1 cells. The mixture of rhu IL-3 plus rHu G-CSF stimulated proliferation to the same extent as did rhu IL-3 alone. The IL-3:G-CSF hybrid growth factor induced a dose response similar to that observed with IL-3.

G-CSF bioactivity of the IL-3:G-CSF hybrid growth factor. To evaluate the biological function of the G-CSF moiety of the IL-3:G-CSF hybrid growth factor, its ability to stimulate proliferation of the murine cell line, NSF-60, was tested. (Figure 10) G-CSF, unlike IL-3 is not species specific, therefore, human G-CSF will actively support growth of murine cells (21). Cells exposed to CHO CM containing no growth factors, supported the proliferation of NSF-60 cells to the same extent as did cells grown in medium alone. The IL-3:G-CSF hybrid growth factor stimulated growth in a dose dependent manner equivalent to that observed with G-CSF.

IL-3 plus G-CSF bioactivity of the IL-3:G-CSF hybrid growth factor. The biological function of the IL-3:G-CSF hybrid growth factor was evaluated by its ability to support growth of an IL-3-, G-CSF-dependent human cell line, AML193. CHO CM containing rHu IL-3, rHu G-CSF and IL-3:G-CSF hybrid growth factor were added to the culture medium. Cell proliferation was monitored by incorporation of radioactivity into the DNA. (Figure 11). Both IL-3 and G-CSF supported growth of this cell line in a dose dependent manner. The two cytokine activities were not synergistic, nor were they additive. The IL-3:G-CSF hybrid growth factor stimulated AML193 proliferation to a greater extent than did the mixture of the two cytokines.

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- 30 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Rosen, Jonathan I.
- (ii) TITLE OF INVENTION: HYBRID GROWTH FACTORS
- (iii) NUMBER OF SEQUENCES: 44
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Robert L. Minier
 - (B) STREET: 1 Johnson & Johnson Plaza
 - (C) CITY: New Brunswick
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 08933
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/589,958
 - (B) FILING DATE: 28-SEP-1990
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Stark, Michael
 - (B) REGISTRATION NUMBER: 32,495
 - (C) REFERENCE/DOCKET NUMBER: BCI-15
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 908-524-2817
 - (B) TELEFAX: 908-524-2808
 - (C) TELEX: 844-481

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

- 31 -

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro	Pro	Leu
			20					25					30		
Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp	Ile	Leu
			35				40					45			
Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	Arg	Ala
	50					55					60				
Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	Lys	Asn
65				70						75				80	
Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	His	Pro
			85					90						95	
Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	Leu	Thr
			100					105					110		
Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	Thr	Thr	Leu
		115					120					125			
Ser	Leu	Ala	Ile	Phe											
			130												

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

- 32 -

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
 1 5 10 15
 Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu
 20 25 30
 Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu
 35 40 45
 Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala
 50 55 60
 Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 1 5 10 15
 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
 20 25 30
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
 35 40 45
 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
 50 55 60
 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
 65 70 75 80
 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
 85 90 95
 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145 150 155 160

Cys Arg Thr Gly Asp Arg
165

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

Cys 1	Asp	Ser	Arg	Val 5	Leu	Glu	Arg	Tyr	Leu 10	Leu	Glu	Ala	Lys	Glu 15	Ala
Glu	Asn	Ile	Thr 20	Thr	Gly	Cys	Ala	Glu 25	His	Cys	Ser	Leu	Asn 30	Glu	Asn
Ile	Thr	Val 35	Pro	Asp	Thr	Lys	Val 40	Asn	Phe	Tyr	Ala	Trp 45	Lys	Arg	Met
Glu	Val 50	Gly	Gln	Gln	Ala	Val 55	Glu	Val	Trp	Gln	Gly 60	Leu	Ala	Leu	Leu
Ser 65	Glu	Ala	Val	Leu	Arg 70	Gly	Gln	Ala	Leu	Leu 75	Val	Asn	Ser	Ser	Gln 80
Pro	Trp	Glu	Pro 85	Leu	Gln	Leu	His	Val	Asp 90	Lys	Ala	Val	Ser	Gly 95	Leu
Arg	Ser	Leu	Thr 100	Thr	Leu	Leu	Arg	Ala 105	Leu	Gly	Ala	Gln	Lys 110	Glu	Ala

Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr
115 120 125

Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
130 135 140

Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys
145 150 155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iv) ANTI-SENSE: NO

Thr 1	Pro	Leu	Gly 5	Pro 5	Ala	Ser	Ser	Leu 10	Pro 10	Gln	Ser	Phe	Leu 15	Leu 15	Lys
Cys	Leu	Glu 20	Gln 20	Val	Arg	Lys	Ile	Gln 25	Gly	Asp	Gly	Ala	Ala 30	Leu 30	Gln
Glu	Lys 35	Leu 35	Cys	Ala	Thr	Tyr 40	Lys 40	Leu	Cys	His	Pro 45	Glu 45	Glu	Leu	Val
Leu 50	Leu 50	Gly	His	Ser	Leu	Gly 55	Ile 55	Pro	Trp	Ala	Pro 60	Leu 60	Ser	Ser	Cys
Pro 65	Ser	Gln	Ala	Leu	Gln 70	Leu 70	Ala	Gly	Cys	Leu 75	Ser 75	Gln	Leu	His 80	Ser 80
Gly	Leu	Phe	Leu 85	Tyr 85	Gln	Gly	Leu	Leu 90	Gln 90	Ala	Leu	Glu	Gly 95	Ile 95	Ser
Pro	Glu	Leu	Gly 100	Pro	Thr	Leu	Asp 105	Thr 105	Leu	Gln	Leu	Asp	Val 110	Ala 110	Asp
Phe	Ala	Thr 115	Thr 115	Ile	Trp	Gln 120	Gln 120	Met	Glu	Glu	Leu 125	Gly 125	Met	Ala	Pro
Ala 130	Leu 130	Gln	Pro	Thr	Gln 135	Gly 135	Ala	Met	Pro	Ala	Phe 140	Ala 140	Ser	Ala	Phe

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Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
 145 150 155 160
 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 165 170

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
 1 5 10 15
 Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu
 20 25 30
 Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu
 35 40 45
 Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala
 50 55 60
 Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys Asn
 65 70 75 80
 Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His Pro
 85 90 95
 Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu Thr
 100 105 110
 Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr Leu
 115 120 125
 Ser Leu Ala Ile Phe Leu Asp Met Ala Pro Pro Arg Leu Ile Cys Asp
 130 135 140
 Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
 145 150 155 160

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Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr
 165 170 175
 Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val
 180 185 190
 Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu
 195 200 205
 Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp
 210 215 220
 Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser
 225 230 235 240
 Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
 245 250 255
 Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp
 260 265 270
 Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys
 275 280 285
 Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
 290 295 300

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
 1 5 10 15
 Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu
 20 25 30
 Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu
 35 40 45

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Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala
 50 55 60
 Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys Asn
 65 70 75 80
 Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His Pro
 85 90 95
 Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu Thr
 100 105 110
 Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr Leu
 115 120 125
 Ser Leu Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140
 Gly Gly Ser Ala Leu Ala Ile Phe Leu Asp Met Ala Pro Pro Arg Leu
 145 150 155 160
 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 165 170 175
 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 180 185 190
 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 195 200 205
 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 210 215 220
 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 225 230 235 240
 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 245 250 255
 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 260 265 270
 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 275 280 285
 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 290 295 300
 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 305 310 315 320
 Arg

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
1           5           10           15
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
20          25          30
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
35          40          45
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
50          55          60
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65          70          75          80
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
85          90          95
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
100         105         110
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
115        120        125
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
130        135        140
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145        150        155        160
Cys Arg Thr Gly Asp Arg Ala Ala Ala Met Ala Pro Met Thr Gln Thr
165        170        175
Thr Ser Leu Lys Thr Ser Trp Val Asn Cys Ser Asn Met Ile Asp Glu
180        185        190

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Ile Ile Thr His Leu Lys Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn
 195 200 205
 Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu Met Glu Asn Asn Leu Arg
 210 215 220
 Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala Val Lys Ser Leu Gln Asn
 225 230 235 240
 Ala Ser Ala Ile Glu Ser Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro
 245 250 255
 Leu Ala Thr Ala Ala Pro Thr Arg His Pro Ile His Ile Lys Asp Gly
 260 265 270
 Asp Trp Asn Glu Phe Arg Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu
 275 280 285
 Glu Asn Ala Gln Ala Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe
 290 295 300

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 1 5 10 15
 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
 20 25 30
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
 35 40 45
 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
 50 55 60
 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
 65 70 75 80

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Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
 85 90 95
 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 100 105 110
 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
 115 120 125
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 130 135 140
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 145 150 155 160
 Cys Arg Thr Gly Asp Arg Ala Ala Ala Ser Gly Gly Gly Gly Ser Gly
 165 170 175
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ala Met Ala Pro Met
 180 185 190
 Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys Ser Asn Met
 195 200 205
 Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu Pro Leu Leu
 210 215 220
 Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu Met Glu Asn
 225 230 235 240
 Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala Val Lys Ser
 245 250 255
 Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys Asn Leu Leu Pro
 260 265 270
 Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His Pro Ile His Ile
 275 280 285
 Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu Thr Phe Tyr Leu
 290 295 300
 Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr Leu Ser Leu Ala
 305 310 315 320
 Ile Phe

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro	Pro	Leu
			20					25					30		
Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp	Ile	Leu
		35					40					45			
Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	Arg	Ala
	50					55					60				
Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	Lys	Asn
65				70					75					80	
Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	His	Pro
			85					90					95		
Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	Leu	Thr
			100					105					110		
Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	Thr	Thr	Leu
		115					120					125			
Ser	Leu	Ala	Ile	Phe	Leu	Glu	Ala	Ala	Ala	Ser	Leu	Pro	Ala	Met	Thr
		130				135					140				
Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Cys
145					150					155				160	
Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu
			165					170					175		
Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu
			180				185						190		
Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro
		195				200					205				
Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly
	210					215					220				

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Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
 225 230 235 240

Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
 245 250 255

Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala
 260 265 270

Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
 275 280 285

Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu
 290 295 300

Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 305 310 315

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 14..977

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 71..977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATTGCCGCC ACC ATG AGC CGC CTG CCC GTC CTG CTC CTG CTC CAA CTC 49
 Met Ser Arg Leu Pro Val Leu Leu Leu Gln Leu
 -19 -15 -10

CTG GTC CGC CCC GGA CTC CAA GCT CCC ATG ACC CAG ACA ACT AGT TTG 97
 Leu Val Arg Pro Gly Leu Gln Ala Pro Met Thr Gln Thr Thr Ser Leu
 -5 1 5

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AAG Lys 10	ACA Thr	AGC Ser	TGG Trp	GTT Val	AAC Asn 15	TGC Cys	TCT Ser	AAC Asn	ATG Met 20	ATC Ile	GAT Asp	GAA Glu	ATT Ile	ATA Ile	ACA Thr 25	145
CAC His	TTA Leu	AAC Asn	GAG Glu	CCA Pro 30	CCT Pro	TTG Leu	CCT Pro	TTG Leu	CTG Leu 35	GAC Asp	TTC Phe	AAC Asn	AAC Asn	CTC Leu 40	AAT Asn	193
GGG Gly	GAA Glu	GAC Asp	CAA Gln 45	GAC Asp	ATT Ile	CTG Leu	ATG Met	GAA Glu 50	AAT Asn	AAC Asn	CTT Leu	CGA Arg	AGG Arg 55	CCA Pro	AAC Asn	241
CTG Leu	GAG Glu	GCA Ala 60	TTC Phe	AAC Asn	AGG Arg	GCT Ala	GTC Val 65	AAG Lys	AGT Ser	TTA Leu	CAG Gln	AAT Asn	GCA Ala	TCA Ser	GCA Ala	289
ATT Ile 75	GAG Glu	AGC Ser	ATT Ile	CTT Leu	AAA Lys 80	AAT Asn	CTC Leu	CTG Leu	CCA Pro	TGT Cys	CTG Leu 85	CCC Pro	CTG Leu	GCC Ala	ACG Thr	337
GCC Ala 90	GCA Ala	CCC Pro	ACG Thr	CGA Arg	CAT His 95	CCA Pro	ATC Ile	CAT His	ATC Ile	AAG Lys 100	GAC Asp	GGT Gly	GAC Asp	TGG Trp	AAT Asn 105	385
GAA Glu	TTC Phe	CGG Arg	AGG Arg	AAA Lys 110	CTG Leu	ACG Thr	TTC Phe	TAT Tyr	CTG Leu 115	AAA Lys	ACC Thr	CTT Leu	GAG Glu	AAT Asn 120	GCG Ala	433
CAG Gln	GCT Ala	CAA Gln	CAG Gln 125	ACG Thr	ACT Thr	TTG Leu	TCG Ser	CTA Leu 130	GCG Ala	ATC Ile	TTT Phe	CTA Leu 135	GAC Asp	ATG Met	GCC Ala	481
CCA Pro	CCA Pro	CGC Arg 140	CTC Leu	ATC Ile	TGT Cys	GAC Asp	AGC Ser 145	CGA Arg	GTC Val	CTG Leu	GAG Glu	AGG Arg	TAC Tyr	CTC Leu	TTG Leu	529
GAG Glu 155	GCC Ala	AAG Lys	GAG Glu	GCC Ala	GAG Glu 160	AAT Asn	ATC Ile	ACG Thr	ACG Thr	GGC Gly	TGT Cys 165	GCT Ala	GAA Glu	CAC His	TGC Cys	577
AGC Ser 170	TTG Leu	AAT Asn	GAG Glu	AAT Asn	ATC Ile 175	ACT Thr	GTC Val	CCA Pro	GAC Asp	ACC Thr 180	AAA Lys	GTT Val	AAT Asn	TTC Phe	TAC Tyr 185	625
GCG Ala	TGG Trp	AAG Lys	AGG Arg	ATG Met 190	GAG Glu	GTC Val	GGC Gly	CAG Gln 195	CAG Gln	GCC Ala	GTA Val	GAA Glu	GTC Val	TGG Trp 200	CAG Gln	673
GGC Gly	CTG Leu	GCC Ala	CTG Leu 205	CTG Leu	TCG Ser	GAA Glu	GCT Ala	GTC Val 210	CTG Leu	CGG Arg	GGC Gly	CAG Gln	GCC Ala 215	CTG Leu	TTG Leu	721

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GTC AAC TCG AGC CAG CCG TGG GAG CCC CTG CAA CTG CAT GTG GAT AAA Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys 220 225 230	769
GCC GTC AGT GGC CTT CGC AGC CTC ACC ACT CTG CTT CGG GCT CTG GGA Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly 235 240 245	817
GCT CAG AAG GAA GCC ATC TCC CCT CCA GAT GCG GCC TCA GCT GCT CCA Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro 250 255 260 265	865
CTC CGA ACA ATC ACT GCT GAC ACT TTC CGC AAA CTC TTC CGA GTC TAC Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr 270 275 280	913
TCC AAT TTC CTC CGG GGA AAG CTG AAG CTG TAC ACA GGG GAG GCA TGC Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys 285 290 295	961
AGG ACA GGG GAC AGA T GATAAGGATC CGAATTC Arg Thr Gly Asp Arg 300	994

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8..998

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 89..998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCGAGCC ATG GGG GTG CAC GAA TGT CCT GCC TGG CTG TGG CTT CTC CTG	49
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu	
-27 -25 -20 -15	

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TCC CTG CTG TCG CTC CCT CTG GGC CTC CCA GTC CTG GGC GCC CCA CCA Ser Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro -10 -5 1	97
CGC CTC ATC TGT GAC AGC CGA GTC CTG GAG AGG TAC CTC TTG GAG GCC Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala 5 10 15	145
AAG GAG GCC GAG AAT ATC ACG ACG GGC TGT GCT GAA CAC TGC AGC TTG Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu 20 25 30 35	193
AAT GAG AAT ATC ACT GTC CCA GAC ACC AAA GTT AAT TTC TAC GCG TGG Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp 40 45 50	241
AAG AGG ATG GAG GTC GGC CAG CAG GCC GTA GAA GTC TGG CAG GGC CTG Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu 55 60 65	289
GCC CTG CTG TCG GAA GCT GTC CTG CGG GGC CAG GCC CTG TTG GTC AAC Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn 70 75 80	337
TCG AGC CAG CCG TGG GAG CCC CTG CAA CTG CAT GTG GAT AAA GCC GTC Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val 85 90 95	385
AGT GGC CTT CGC AGC CTC ACC ACT CTG CTT CGG GCT CTG GGA GCT CAG Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln 100 105 110 115	433
AAG GAA GCC ATC TCC CCT CCA GAT GCG GCC TCA GCT GCT CCA CTC CGA Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg 120 125 130	481
ACA ATC ACT GCT GAC ACT TTC CGC AAA CTC TTC CGA GTC TAC TCC AAT Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn 135 140 145	529
TTC CTC CGG GGA AAG CTG AAG CTG TAC ACA GGG GAG GCA TGC AGG ACA Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr 150 155 160	577
GGG GAC AGA GCG GCC GCC ATG GCT CCC ATG ACC CAG ACA ACT AGT TTG Gly Asp Arg Ala Ala Ala Met Ala Pro Met Thr Gln Thr Thr Ser Leu 165 170 175	625
AAG ACA AGC TGG GTT AAC TGC TCT AAC ATG ATC GAT GAA ATT ATA ACA Lys Thr Ser Trp Val Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr 180 185 190 195	673

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CAC TTA AAC GAG CCA CCT TTG CCT TTG CTG GAC TTC AAC AAC CTC AAT His Leu Asn Glu Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn 200 205 210	721
GGG GAA GAC CAA GAC ATT CTG ATG GAA AAT AAC CTT CGA AGG CCA AAC Gly Glu Asp Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn 215 220 225	769
CTG GAG GCA TTC AAC AGG GCT GTC AAG AGT TTA CAG AAT GCA TCA GCA Leu Glu Ala Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala 230 235 240	817
ATT GAG AGC ATT CTT AAA AAT CTC CTG CCA TGT CTG CCC CTG GCC ACG Ile Glu Ser Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr 245 250 255	865
GCC GCA CCC ACG CGA CAT CCA ATC CAT ATC AAG GAC GGT GAC TGG AAT Ala Ala Pro Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn 260 265 270 275	913
GAA TTC CGG AGG AAA CTG ACG TTC TAT CTG AAA ACC CTT GAG AAT GCG Glu Phe Arg Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala 280 285 290	961
CAG GCT CAA CAG ACG ACT TTG TCG CTA GCG ATC TTT T AGTAAGGATC Gln Ala Gln Thr Thr Leu Ser Leu Ala Ile Phe 295 300	1008
CGAATTC	1015

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 14..1021

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 71..1021

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AATTGCCGCC ACC ATG AGC CGC CTG CCC GTC CTG CTC CTG CTC CAA CTC	49
Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu	
-19 -15 -10	
CTG GTC CGC CCC GGA CTC CAA GCT CCC ATG ACC CAG ACA ACT AGT TTG	97
Leu Val Arg Pro Gly Leu Gln Ala Pro Met Thr Gln Thr Thr Ser Leu	
-5 1 5	
AAG ACA AGC TGG GTT AAC TGC TCT AAC ATG ATC GAT GAA ATT ATA ACA	145
Lys Thr Ser Trp Val Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr	
10 15 20 25	
CAC TTA AAC GAG CCA CCT TTG CCT TTG CTG GAC TTC AAC AAC CTC AAT	193
His Leu Asn Glu Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn	
30 35 40	
GGG GAA GAC CAA GAC ATT CTG ATG GAA AAT AAC CTT CGA AGG CCA AAC	241
Gly Glu Asp Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn	
45 50 55	
CTG GAG GCA TTC AAC AGG GCT GTC AAG AGT TTA CAG AAT GCA TCA GCA	289
Leu Glu Ala Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala	
60 65 70	
ATT GAG AGC ATT CTT AAA AAT CTC CTG CCA TGT CTG CCC CTG GCC ACG	337
Ile Glu Ser Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr	
75 80 85	
GCC GCA CCC ACG CGA CAT CCA ATC CAT ATC AAG GAC GGT GAC TGG AAT	385
Ala Ala Pro Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn	
90 95 100 105	
GAA TTC CGG AGG AAA CTG ACG TTC TAT CTG AAA ACC CTT GAG AAT GCG	433
Glu Phe Arg Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala	
110 115 120	
CAG GCT CAA CAG ACG ACT TTG TCG CTA GCG ATC TTT CTA GAA GCG GCC	481
Gln Ala Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe Leu Glu Ala Ala	
125 130 135	
GCA AGC TTA CCT GCC ATG ACC CCC CTG GGC CCT GCC AGC TCC CTG CCC	529
Ala Ser Leu Pro Ala Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro	
140 145 150	
CAG AGC TTC CTG CTC AAG TGC TTA GAG CAA GTG AGG AAG ATC CAG GGC	577
Gln Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly	
155 160 165	
GAT GGC GCA GCG CTC CAG GAG AAG CTG TGT GCC ACC TAC AAG CTG TGC	625
Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys	
170 175 180 185	

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CAC CCC GAG GAG CTG GTG CTG CTC GGA CAC TCT CTG GGC ATC CCC TGG His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp 190 195 200	673
GCT CCC CTG AGC TCC TGC CCC AGC CAG GCC CTG CAG CTG GCA GGC TGC Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys 205 210 215	721
TTG AGC CAA CTC CAT AGC GGC CTT TTC CTC TAC CAG GGG CTC CTG CAG Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln 220 225 230	769
GCC CTG GAA GGG ATA TCC CCC GAG TTG GGT CCC ACC TTG CAC ACA CTG Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu His Thr Leu 235 240 245	817
CAG CTG GAC GTC GCC GAC TTT GCC ACC ACC ATC TGG CAG CAG ATG GAA Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu 250 255 260 265	865
GAA CTG GGA ATG GCC CCT GCC CTG CAG CCC ACC CAG GGT GCC ATG CCG Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro 270 275 280	913
GCC TTC GCC TCT GCT TTC CAG CGC CGG GCA GGA GGG GTC CTG GTT GCT Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala 285 290 295	961
AGC CAT CTG CAG AGC TTC CTG GAG GTG TCG TAC CGC GTT CTA CGC CAC Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His 300 305 310	1009
CTT GCG CAG CCC TGATAAGGAT CCGAATTC Leu Ala Gln Pro 315	1039

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

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(A) NAME/KEY: CDS
 (B) LOCATION: 14..1033

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 71..1033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATTGCCGCC ACC ATG AGC CGC CTG CCC GTC CTG CTC CTG CTC CAA CTC	49
Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu	
-19 -15 -10	
CTG GTC CGC CCC GGA CTC CAA GCT CCC ATG ACC CAG ACA ACT AGT TTG	97
Leu Val Arg Pro Gly Leu Gln Ala Pro Met Thr Gln Thr Thr Ser Leu	
-5 1 5	
AAG ACA AGC TGG GTT AAC TGC TCT AAC ATG ATC GAT GAA ATT ATA ACA	145
Lys Thr Ser Trp Val Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr	
10 15 20 25	
CAC TTA AAC GAG CCA CCT TTG CCT TTG CTG GAC TTC AAC AAC CTC AAT	193
His Leu Asn Glu Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn	
30 35 40	
GGG GAA GAC CAA GAC ATT CTG ATG GAA AAT AAC CTT CGA AGG CCA AAC	241
Gly Glu Asp Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn	
45 50 55	
CTG GAG GCA TTC AAC AGG GCT GTC AAG AGT TTA CAG AAT GCA TCA GCA	289
Leu Glu Ala Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala	
60 65 70	
ATT GAG AGC ATT CTT AAA AAT CTC CTG CCA TGT CTG CCC CTG GCC ACG	337
Ile Glu Ser Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr	
75 80 85	
GCC GCA CCC ACG CGA CAT CCA ATC CAT ATC AAG GAC GGT GAC TGG AAT	385
Ala Ala Pro Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn	
90 95 100 105	
GAA TTC CGG AGG AAA CTG ACG TTC TAT CTG AAA ACC CTT GAG AAT GCG	433
Glu Phe Arg Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala	
110 115 120	
CAG GCT CAA CAG ACG ACT TTG TCG CTA GCG TCC GGA GGC GGT GGC TCG	481
Gln Ala Gln Gln Thr Thr Leu Ser Leu Ala Ser Gly Gly Gly Gly Ser	
125 130 135	
GGC GGT GGC GGC TCG GGT GGC GGC GGC TCT GCG CTA GCG ATC TTT CTA	529
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Ala Ile Phe Leu	
140 145 150	

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GAC ATG GCC CCA CCA CGC CTC ATC TGT GAC AGC CGA GTC CTG GAG AGG Asp Met Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg 155 160 165	577
TAC CTC TTG GAG GCC AAG GAG GCC GAG AAT ATC ACG ACG GGC TGT GCT Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala 170 175 180 185	625
GAA CAC TGC AGC TTG AAT GAG AAT ATC ACT GTC CCA GAC ACC AAA GTT Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val 190 195 200	673
AAT TTC TAC GCG TGG AAG AGG ATG GAG GTC GGC CAG CAG GCC GTA GAA Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu 205 210 215	721
GTC TGG CAG GGC CTG GCC CTG CTG TCG GAA GCT GTC CTG CGG GGC CAG Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln 220 225 230	769
GCC CTG TTG GTC AAC TCG AGC CAG CCG TGG GAG CCC CTG CAA CTG CAT Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His 235 240 245	817
GTG GAT AAA GCC GTC AGT GGC CTT CGC AGC CTC ACC ACT CTG CTT CGG Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg 250 255 260 265	865
GCT CTG GGA GCT CAG AAG GAA GCC ATC TCC CCT CCA GAT GCG GCC TCA Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser 270 275 280	913
GCT GCT CCA CTC CGA ACA ATC ACT GCT GAC ACT TTC CGC AAA CTC TTC Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe 285 290 295	961
CGA GTC TAC TCC AAT TTC CTC CGG GGA AAG CTG AAG CTG TAC ACA GGG Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly 300 305 310	1009
GAG GCA TGC AGG ACA GGG GAC AGA TGATAAGGAT CCGAATTC Glu Ala Cys Arg Thr Gly Asp Arg 315 320	1051

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 8..1054

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 89..1054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGAGCC	ATG	GGG	GTG	CAC	GAA	TGT	CCT	GCC	TGG	CTG	TGG	CTT	CTC	CTG	49	
	Met	Gly	Val	His	Glu	Cys	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Leu		
	-27		-25					-20					-15			
TCC	CTG	CTG	TCG	CTC	CCT	CTG	GGC	CTC	CCA	GTC	CTG	GGC	GCC	CCA	CCA	97
Ser	Leu	Leu	Ser	Leu	Pro	Leu	Gly	Leu	Pro	Val	Leu	Gly	Ala	Pro	Pro	
			-10					-5					1			
CGC	CTC	ATC	TGT	GAC	AGC	CGA	GTC	CTG	GAG	AGG	TAC	CTC	TTG	GAG	GCC	145
Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	
	5					10				15						
AAG	GAG	GCC	GAG	AAT	ATC	ACG	ACG	GGC	TGT	GCT	GAA	CAC	TGC	AGC	TTG	193
Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	
	20				25				30						35	
AAT	GAG	AAT	ATC	ACT	GTC	CCA	GAC	ACC	AAA	GTT	AAT	TTC	TAC	GCG	TGG	241
Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	
			40					45						50		
AAG	AGG	ATG	GAG	GTC	GGC	CAG	CAG	GCC	GTA	GAA	GTC	TGG	CAG	GGC	CTG	289
Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	
			55					60					65			
GCC	CTG	CTG	TCG	GAA	GCT	GTC	CTG	CGG	GGC	CAG	GCC	CTG	TTG	GTC	AAC	337
Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	
			70					75					80			
TCG	AGC	CAG	CCG	TGG	GAG	CCC	CTG	CAA	CTG	CAT	GTG	GAT	AAA	GCC	GTC	385
Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	
	85					90					95					
AGT	GGC	CTT	CGC	AGC	CTC	ACC	ACT	CTG	CTT	CGG	GCT	CTG	GGA	GCT	CAG	433
Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	
	100				105					110					115	

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AAG GAA GCC ATC TCC CCT CCA GAT GCG GCC TCA GCT GCT CCA CTC CGA Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg 120 125 130	481
ACA ATC ACT GCT GAC ACT TTC CGC AAA CTC TTC CGA GTC TAC TCC AAT Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn 135 140 145	529
TTC CTC CGG GGA AAG CTG AAG CTG TAC ACA GGG GAG GCA TGC AGG ACA Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr 150 155 160	577
GGG GAC AGA GCG GCC GCC TCC GGA GGC GGT GGC TCG GGC GGT GGC GGC Gly Asp Arg Ala Ala Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly 165 170 175	625
TCG GGT GGC GGC GGC TCT GCG GCC GCC ATG GCT CCC ATG ACC CAG ACA Ser Gly Gly Gly Gly Ser Ala Ala Ala Met Ala Pro Met Thr Gln Thr 180 185 190 195	673
ACT AGT TTG AAG ACA AGC TGG GTT AAC TGC TCT AAC ATG ATC GAT GAA Thr Ser Leu Lys Thr Ser Trp Val Asn Cys Ser Asn Met Ile Asp Glu 200 205 210	721
ATT ATA ACA CAC TTA AAC GAG CCA CCT TTG CCT TTG CTG GAC TTC AAC Ile Ile Thr His Leu Asn Glu Pro Pro Leu Pro Leu Leu Asp Phe Asn 215 220 225	769
AAC CTC AAT GGG GAA GAC CAA GAC ATT CTG ATG GAA AAT AAC CTT CGA Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu Met Glu Asn Asn Leu Arg 230 235 240	817
AGG CCA AAC CTG GAG GCA TTC AAC AGG GCT GTC AAG AGT TTA CAG AAT Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala Val Lys Ser Leu Gln Asn 245 250 255	865
GCA TCA GCA ATT GAG AGC ATT CTT AAA AAT CTC CTG CCA TGT CTG CCC Ala Ser Ala Ile Glu Ser Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro 260 265 270 275	913
CTG GCC ACG GCC GCA CCC ACG CGA CAT CCA ATC CAT ATC AAG GAC GGT Leu Ala Thr Ala Ala Pro Thr Arg His Pro Ile His Ile Lys Asp Gly 280 285 290	961
GAC TGG AAT GAA TTC CGG AGG AAA CTG ACG TTC TAT CTG AAA ACC CTT Asp Trp Asn Glu Phe Arg Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu 295 300 305	1009
GAG AAT GCG CAG GCT CAA CAG ACG ACT TTG TCG CTA GCG ATC TTT Glu Asn Ala Gln Ala Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe 310 315 320	1054
TAGTAAGGAT CCGAATTC	1072

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 10..411

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 13..411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAGCTTACC ATG GCT CCC ATG ACC CAG ACA ACT AGT TTG AAG ACA AGC	48
Met Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser	
-1 1 5 10	
TGG GTT AAC TGC TCT AAC ATG ATC GAT GAA ATT ATA ACA CAC TTA AAC	96
Trp Val Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Asn	
15 20 25	
GAG CCA CCT TTG CCT TTG CTG GAC TTC AAC AAC CTC AAT GGG GAA GAC	144
Glu Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp	
30 35 40	
CAA GAC ATT CTG ATG GAA AAT AAC CTT CGA AGG CCA AAC CTG GAG GCA	192
Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala	
45 50 55 60	
TTC AAC AGG GCT GTC AAG AGT TTA CAG AAT GCA TCA GCA ATT GAG AGC	240
Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser	
65 70 75	
ATT CTT AAA AAT CTC CTG CCA TGT CTG CCC CTG GCC ACG GCC GCA CCC	288
Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro	
80 85 90	
ACG CGA CAT CCA ATC CAT ATC AAG GAC GGT GAC TGG AAT GAA TTC CGG	336
Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg	
95 100 105	

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AGG AAA CTG ACG TTC TAT CTG AAA ACC CTT GAG AAT GCG CAG GCT CAA 384
 Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
 110 115 120

CAG ACG ACT TTG TCG CTA GCG ATC TTT TAGTAAGGAT CCGAATTC 429
 Gln Thr Thr Leu Ser Leu Ala Ile Phe
 125 130

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 14..514

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 17..514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAGCTTACCT GCC ATG GCC CCA CCA CGC CTC ATC TGT GAC AGC CGA GTC 49
 Met Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val
 -1 1 5 10

CTG GAG AGG TAC CTC TTG GAG GCC AAG GAG GCC GAG AAT ATC ACG ACG 97
 Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
 15 20 25

GGC TGT GCT GAA CAC TGC AGC TTG AAT GAG AAT ATC ACT GTC CCA GAC 145
 Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp
 30 35 40

ACC AAA GTT AAT TTC TAC GCG TGG AAG AGG ATG GAG GTC GGC CAG CAG 193
 Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln
 45 50 55

GCC GTA GAA GTC TGG CAG GGC CTG GCC CTG CTG TCG GAA GCT GTC CTG 241
 Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
 60 65 70 75

- 55 -

CGG GGC CAG GCC CTG TTG GTC AAC TCG AGC CAG CCG TGG GAG CCC CTG	289
Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu	
80 85 90	
CAA CTG CAT GTG GAT AAA GCC GTC AGT GGC CTT CGC AGC CTC ACC ACT	337
Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr	
95 100 105	
CTG CTT CGG GCT CTG GGA GCT CAG AAG GAA GCC ATC TCC CCT CCA GAT	385
Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp	
110 115 120	
GCG GCC TCA GCT GCT CCA CTC CGA ACA ATC ACT GCT GAC ACT TTC CGC	433
Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg	
125 130 135	
AAA CTC TTC CGA GTC TAC TCC AAT TTC CTC CGG GGA AAG CTG AAG CTG	481
Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu	
140 145 150 155	
TAC ACA GGG GAG GCA TGC AGG ACA GGG GAC AG ATGATAAGGA TCCGAATTC	532
Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp	
160 165	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 14..538

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 17..538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AAGCTTACCT GCC ATG ACC CCC CTG GGC CCT GCC AGC TCC CTG CCC CAG	49
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln	
-1 1 5 10	

- 56 -

AGC TTC CTG CTC AAG TGC TTA GAG CAA GTG AGG AAG ATC CAG GGC GAT Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp 15 20 25	97
GGC GCA GCG CTC CAG GAG AAG CTG TGT GCC ACC TAC AAG CTG TGC CAC Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His 30 35 40	145
CCC GAG GAG CTG GTG CTG CTC GGA CAC TCT CTG GGC ATC CCC TGG GCT Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala 45 50 55	193
CCC CTG AGC TCC TGC CCC AGC CAG GCC CTG CAG CTG GCA GGC TGC TTG Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu 60 65 70 75	241
AGC CAA CTC CAT AGC GGC CTT TTC CTC TAC CAG GGG CTC CTG CAG GCC Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala 80 85 90	289
CTG GAA GGG ATA TCC CCC GAG TTG GGT CCC ACC TTG CAC ACA CTG CAG Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu His Thr Leu Gln 95 100 105	337
CTG GAC GTC GCC GAC TTT GCC ACC ACC ATC TGG CAG CAG ATG GAA GAA Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu 110 115 120	385
CTG GGA ATG GCC CCT GCC CTG CAG CCC ACC CAG GGT GCC ATG CCG GCC Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala 125 130 135	433
TTC GCC TCT GCT TTC CAG CGC CGG GCA GGA GGG GTC CTG GTT GCT AGC Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser 140 145 150 155	481
CAT CTG CAG AGC TTC CTG GAG GTG TCG TAC CGC GTT CTA CGC CAC CTT His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu 160 165 170	529
GCG CAG CCC TGATAAGGAT CCGAATTC Ala Gln Pro	556

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AATTGCCGCC ACCATGAGCC GCCTGCCCGT CCTGCTCCT

39

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCTCCAACCTC CTGGTCCGCC CCGGACTCCA AGCTCCCATG ACCCAGACAA

50

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTAGTTGTCT GGGTCATGGG AGCTTGAGT CCGGGGCGG

39

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(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCAGGAGTT GGAGCAGGAG CAGGACGGGC AGGCGGCTCA TGGTGGCGGC

50

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTAGCGATCT TTCTAGA

17

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: NO

- 59 -

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CATGTCTAGA AAGATCG

17

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTAGCGTCCG GAGGCGGTGG CTCGGGCGGT GGCGGCTCGG GTGGCGGCGG CTCTGCG

57

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTAGCGCAGA GCCGCCGCCA CCGCAGCCGC CACCGCCCGA GCCACCGCCT CCGGACG

57

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTGTCGCTAG CGTCCGGAGG C

21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTAGAAGCGG CCGCA

15

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTCGCCGGCG TTCGA

15

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCGAGCCATG GGGGTGCACG AATGTCCT

28

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCTGGCTGT GGCTTCTCCT GTCCCTGCTG TC

32

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCTCCCTCTG GGCCTCCCAG TCCTGGGCTG CA

32

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCCAGGACT GGGAGGCCCA GAGGGA

26

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(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCGACAGCAG GGACAGGAGA AGCCACAGCC AGGCAGGACA TT

42

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGTGCACCCC CATGGC

16

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCCCCACCAC GCCTCATCTG T

21

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCGGAT CCTTATCATC T

21

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTAGTCTCTA GAATGGGGGT CCACGAATGT

30

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGCCATGGCG GCCGCTCTGT CCCCTGTCCT

30

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GACAGAGCGG CCGCCATGGC TCCCATGACC

30

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GAATTCGGAT CCTTACTAAA AGATCGCTAG

30

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(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGCCGCTTCC GGAGGCGGTG GCTCGGGCGG TGGCGGCTCG GGTGGCGGCG GCTCTGC 57

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGCCGCAGAG CCGCCGCCAC CCGAGCCGCC ACCGCCCAG CCACCGCCTC CGGCAGC 57

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What is claimed is:

1. A recombinant hematopoietic molecule comprising at least a portion of a first hematopoietic molecule having early myeloid differentiation activity and at least a portion of a second hematopoietic molecule having late myeloid differentiation activity, said recombinant hematopoietic molecule having early myeloid differentiation activity associated with said first hematopoietic molecule and late myeloid differentiation activity associated with said second hematopoietic molecule.

2. A recombinant hematopoietic molecule of claim 1 wherein the first hematopoietic molecule is selected from the group consisting of IL-3 and GM-CSF.

3. A recombinant hematopoietic molecule of claim 1 wherein the second hematopoietic molecule is selected from the group consisting of Epo, G-CSF, IL-5 and M-CSF.

4. A recombinant hematopoietic molecule of claim 1 wherein the portion of the first hematopoietic molecule is linked to the portion of the second hematopoietic molecule by an amino acid linker sequence of at least two amino acid residues.

5. A recombinant hematopoietic molecule of claim 1 comprising SEQ ID NO: 1.

6. A recombinant hematopoietic molecule of claim 1 comprising an amino acid sequence contained within SEQ ID NO: 2.

7. A recombinant hematopoietic molecule of claim 1 comprising SEQ ID NO: 3.

8. A recombinant hematopoietic molecule of claim 1 comprising an amino acid sequence contained within SEQ ID NO: 4.

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9. A recombinant hematopoietic molecule of claim 1 comprising
SEQ ID NO: 5.

5 10. A recombinant hematopoietic molecule of claim 1 wherein the
first hematopoietic molecule is IL-3 and the second hematopoietic
molecule is Epo.

10 11. A recombinant hematopoietic molecule of claim 10 wherein the
first hematopoietic molecule comprises the amino portion and the
second hematopoietic molecule comprises the carboxy portion of the
recombinant hematopoietic molecule.

15 12. A recombinant hematopoietic molecule of claim 11 which
comprises SEQ ID NO: 6.

13. A recombinant hematopoietic molecule of claim 11 which
comprises SEQ ID NO: 7.

20 14. A recombinant hematopoietic molecule of claim 10 wherein the
first hematopoietic molecule comprises the carboxy portion and the
second hematopoietic molecule comprises the amino portion of the
recombinant hematopoietic molecule.

25 15. A recombinant hematopoietic molecule of claim 14 which
comprises SEQ ID NO: 8.

16. A recombinant hematopoietic molecule of claim 14 which
comprises SEQ ID NO: 9.

30 17. A recombinant hematopoietic molecule of claim 1 wherein the
first hematopoietic molecule is IL-3 and the second hematopoietic
molecule is G-CSF

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18. A recombinant hematopoietic molecule of claim 17 wherein the first hematopoietic molecule comprises the amino portion and the second hematopoietic molecule comprises the carboxy portion of the recombinant hematopoietic molecule.

5

19. A recombinant hematopoietic molecule of claim 18 which comprises SEQ ID NO: 10.

20. A nucleic acid molecule which encodes the recombinant hematopoietic molecule of claim 1.

10

21. An expression vector which comprises the nucleic acid molecule of claim 20.

22. A host cell transformed with the expression vector of claim 19.

15

23. A host cell of claim 22 which comprises a mammalian cell.

20

24. A method for producing a recombinant hematopoietic molecule comprising at least a portion of a first hematopoietic molecule having early myeloid differentiation activity and at least a portion of a second hematopoietic molecule having late myeloid differentiation activity, which comprises culturing a host cell of claim 22 under suitable conditions so as to allow the expression of such recombinant hematopoietic molecule, and recovering such recombinant hematopoietic molecule.

25

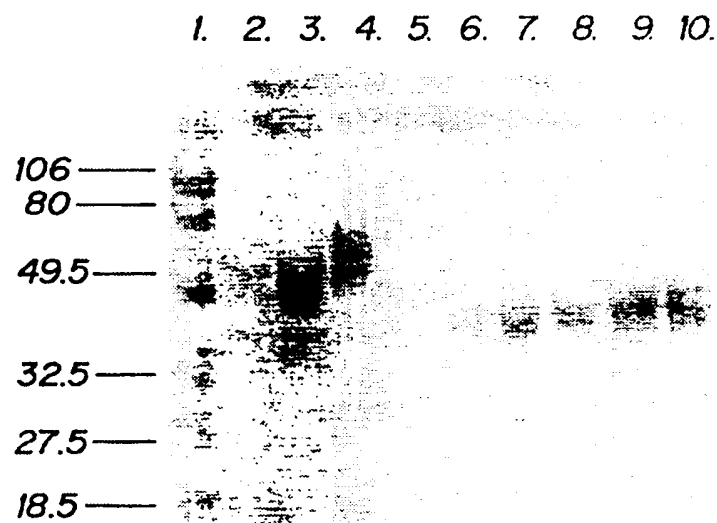
25. A pharmaceutical composition which comprises a recombinant hematopoietic molecule of claim 1 and a pharmaceutically acceptable carrier.

30

26. A method for promoting hematopoiesis in a patient which comprises administering to such patient a pharmaceutical composition of claim 25.

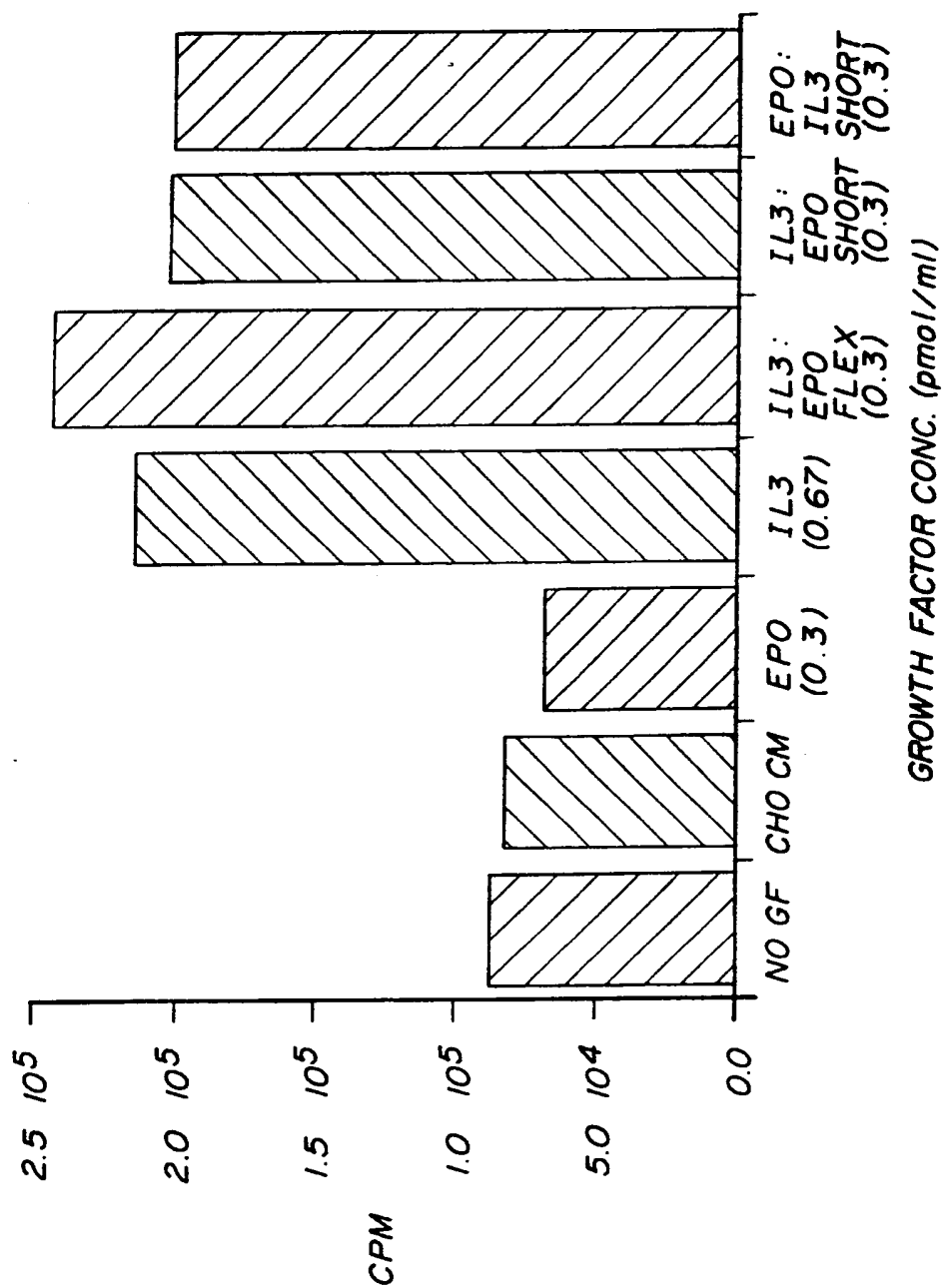
35

FIG-1



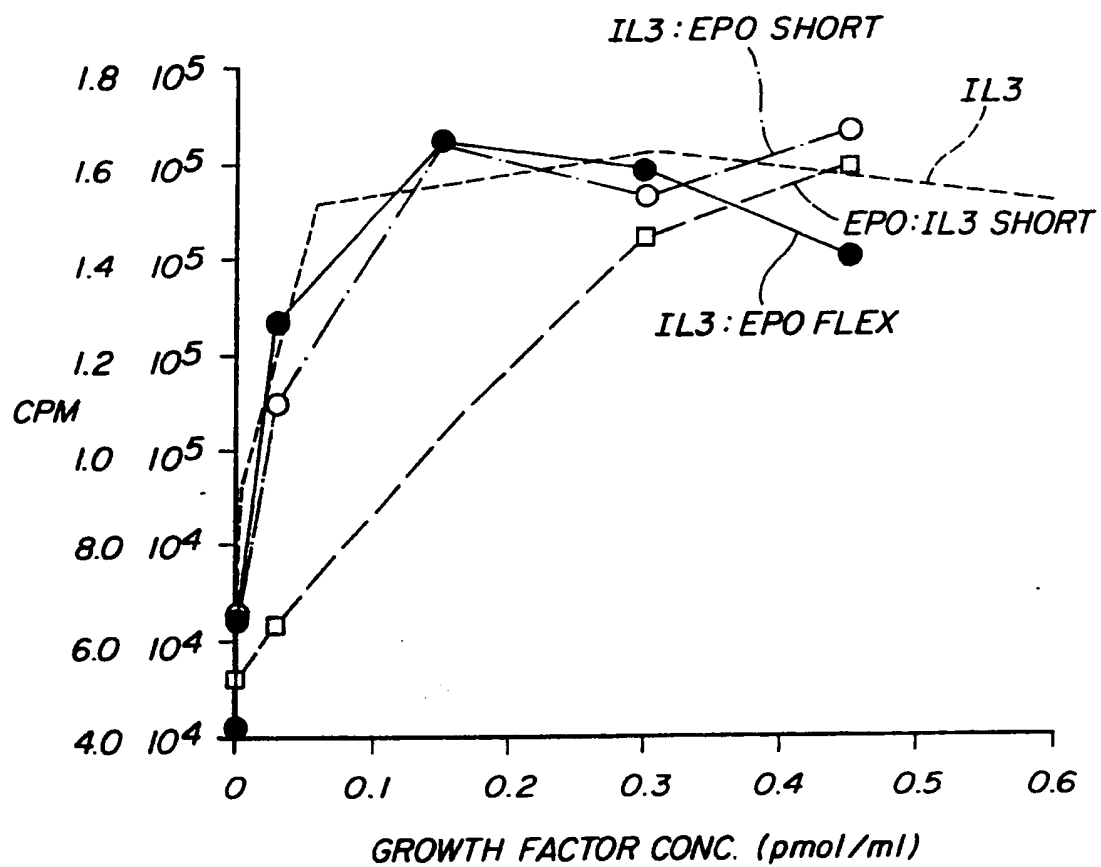
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FIG-2



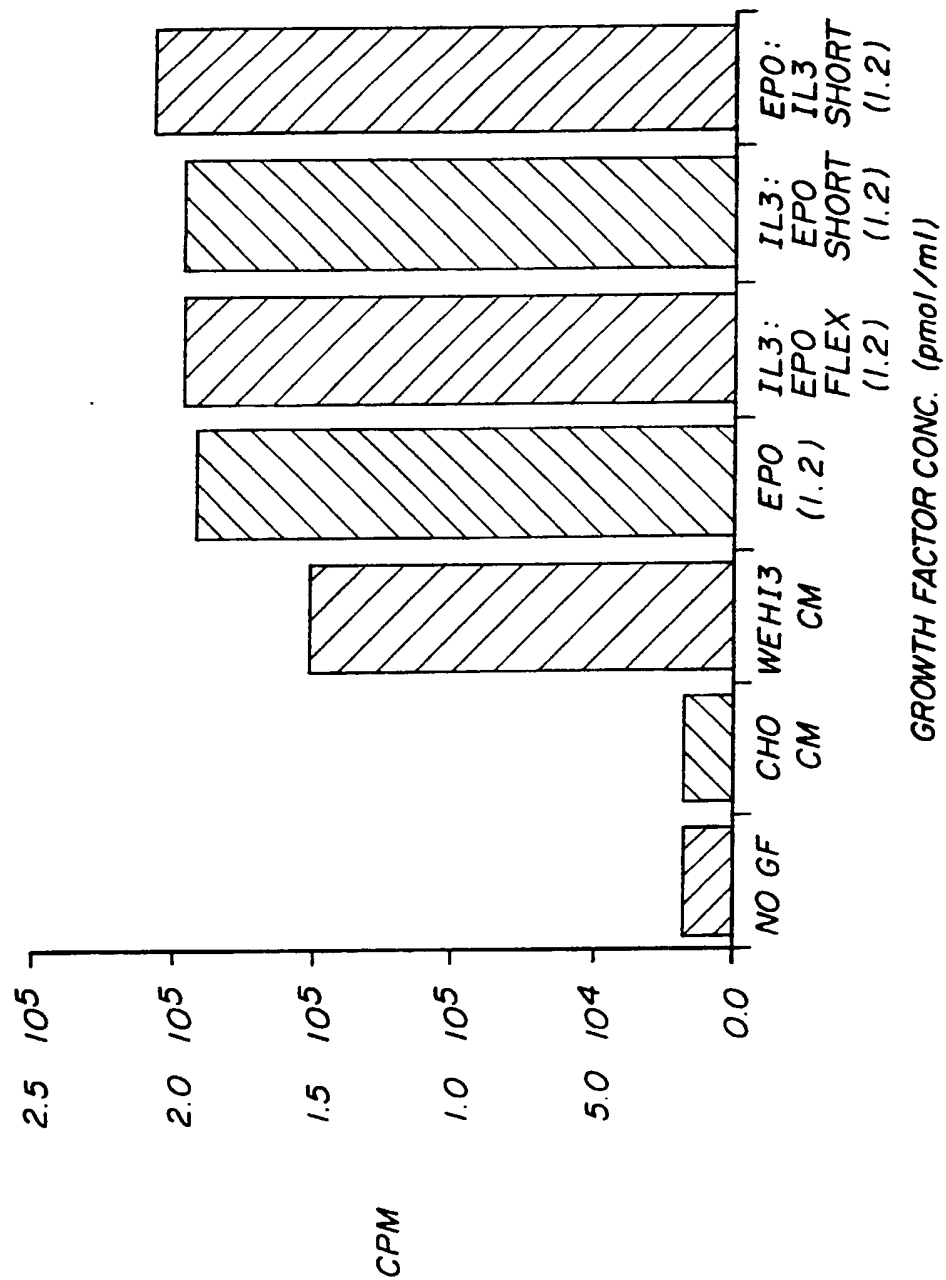
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FIG-3



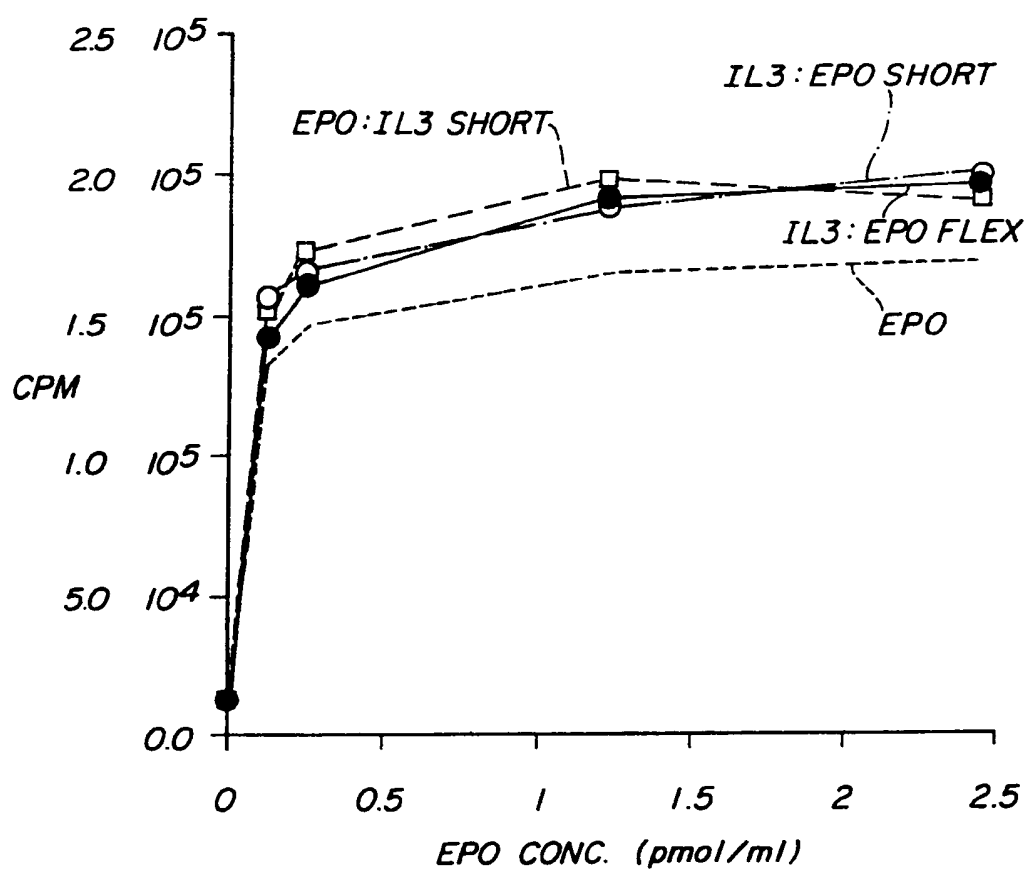
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FIG-4



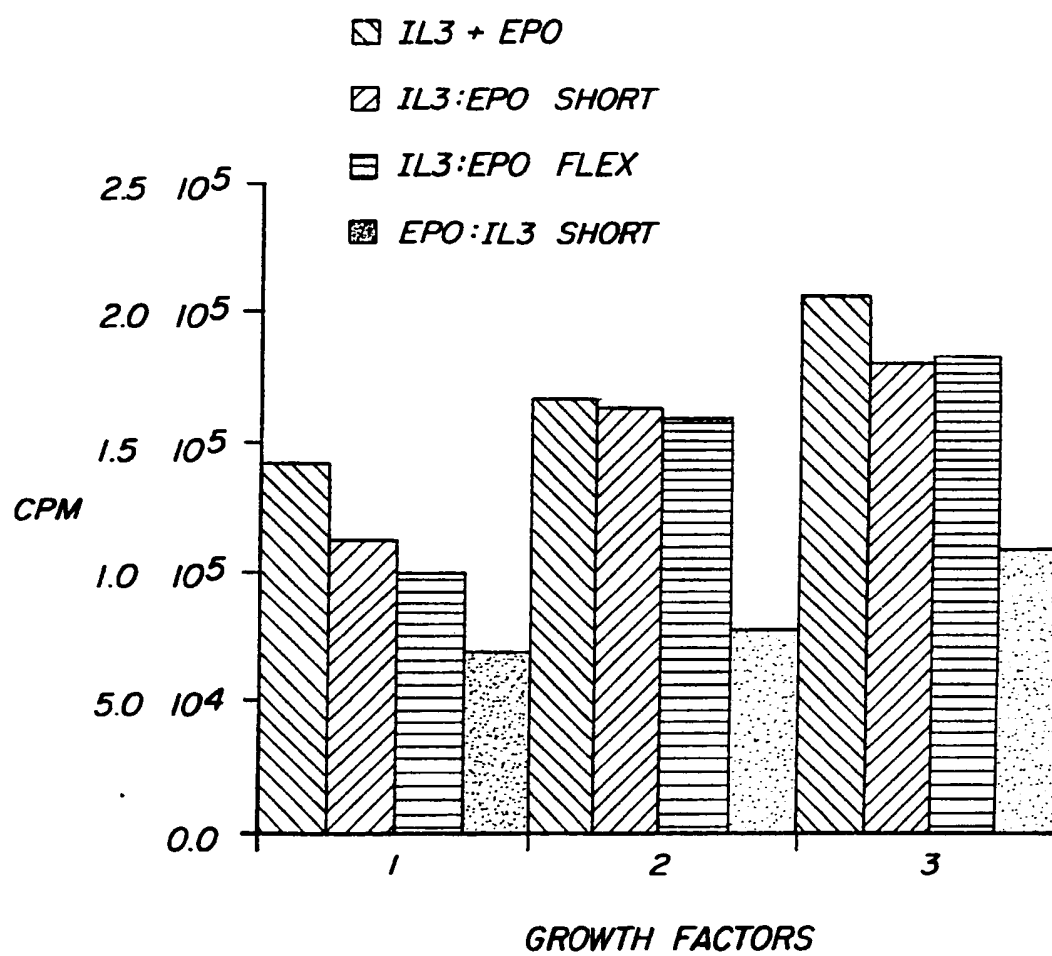
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FIG-5



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FIG-6



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FIG-7A

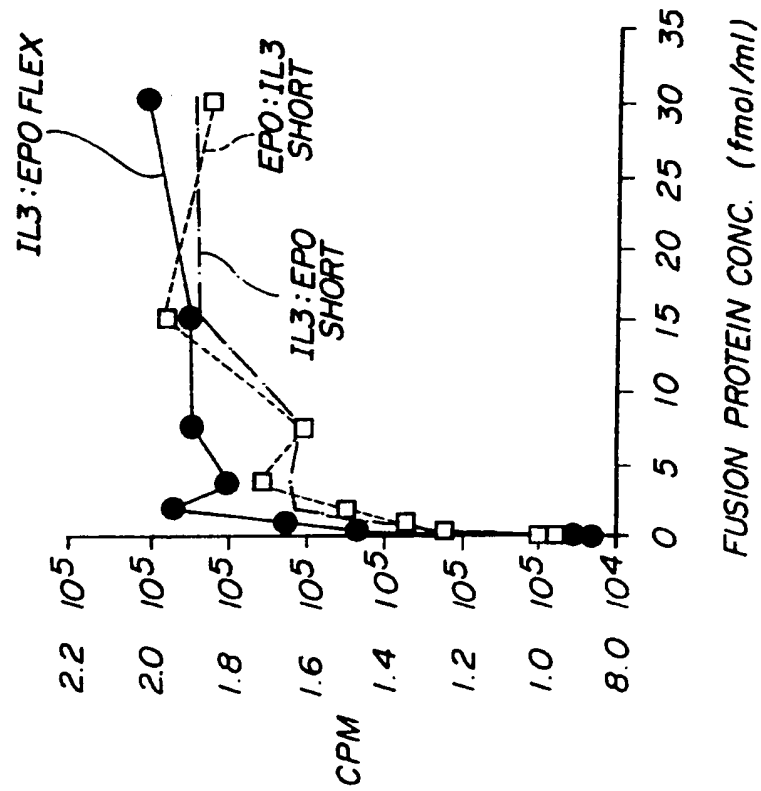


FIG-7B

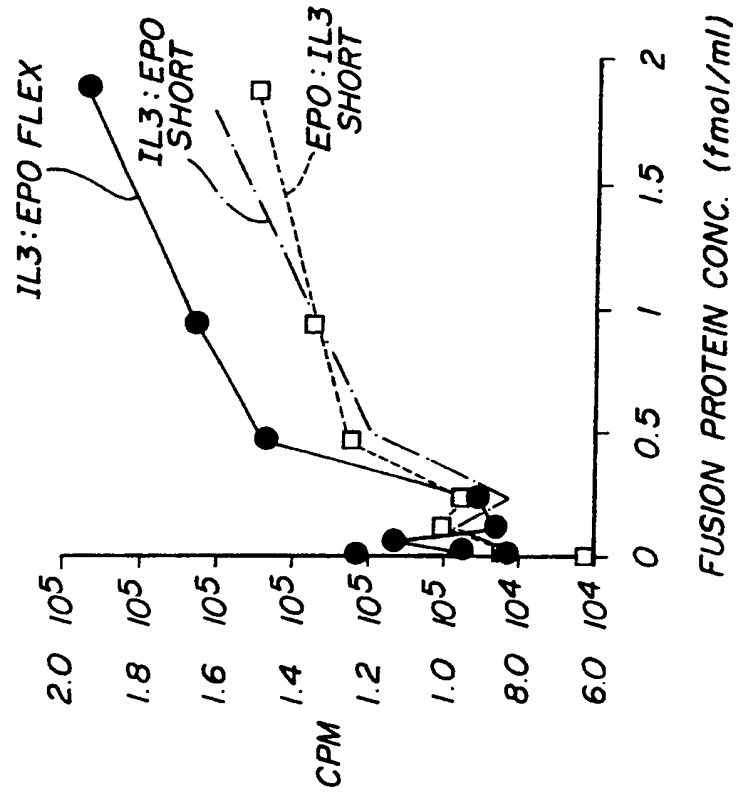


FIG-8A

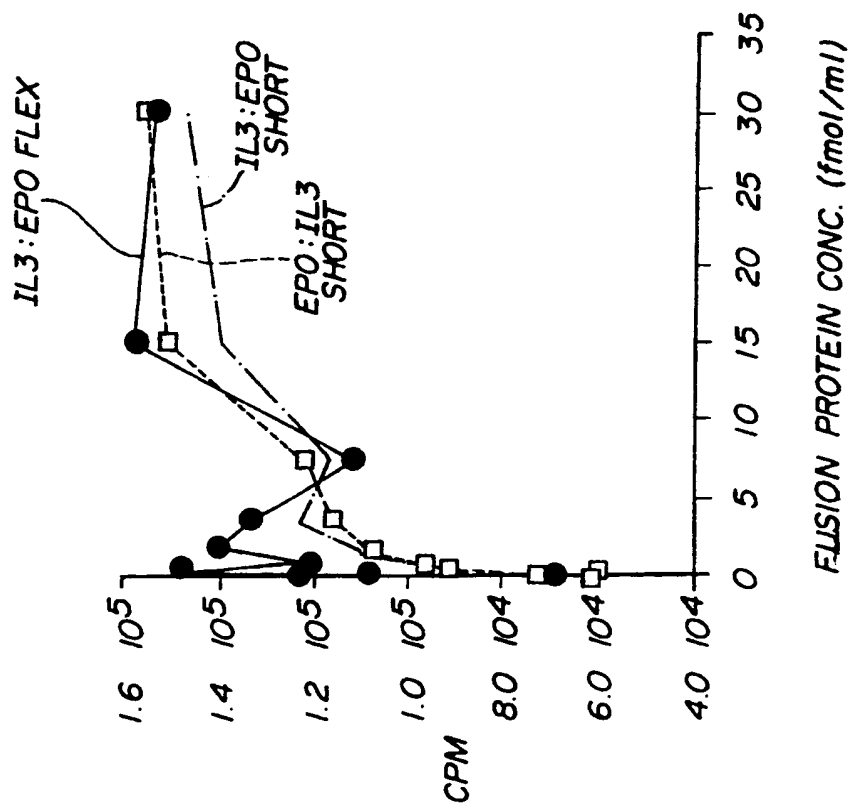
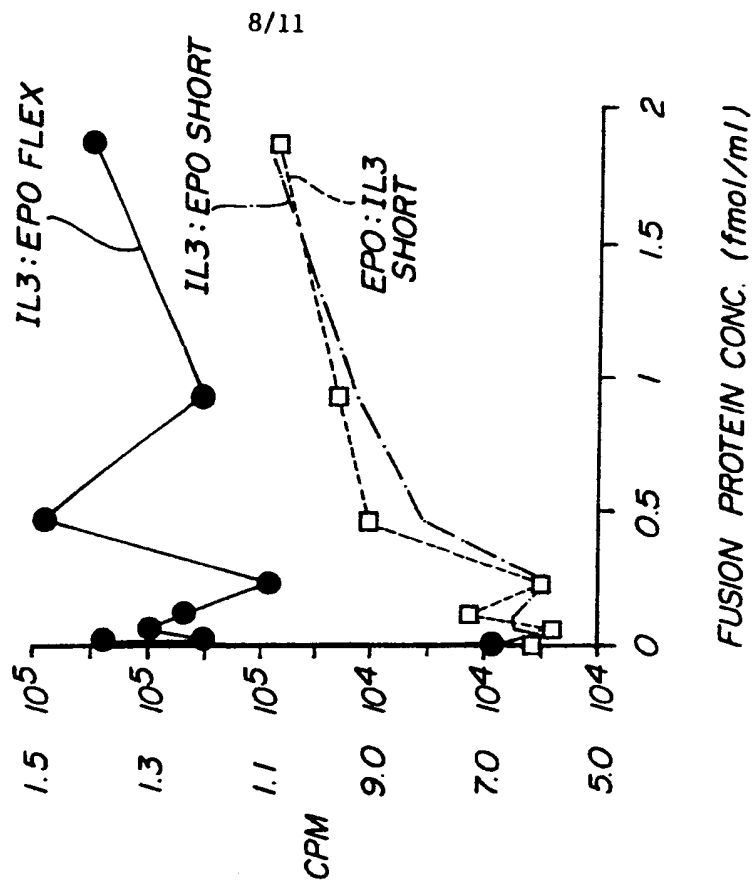


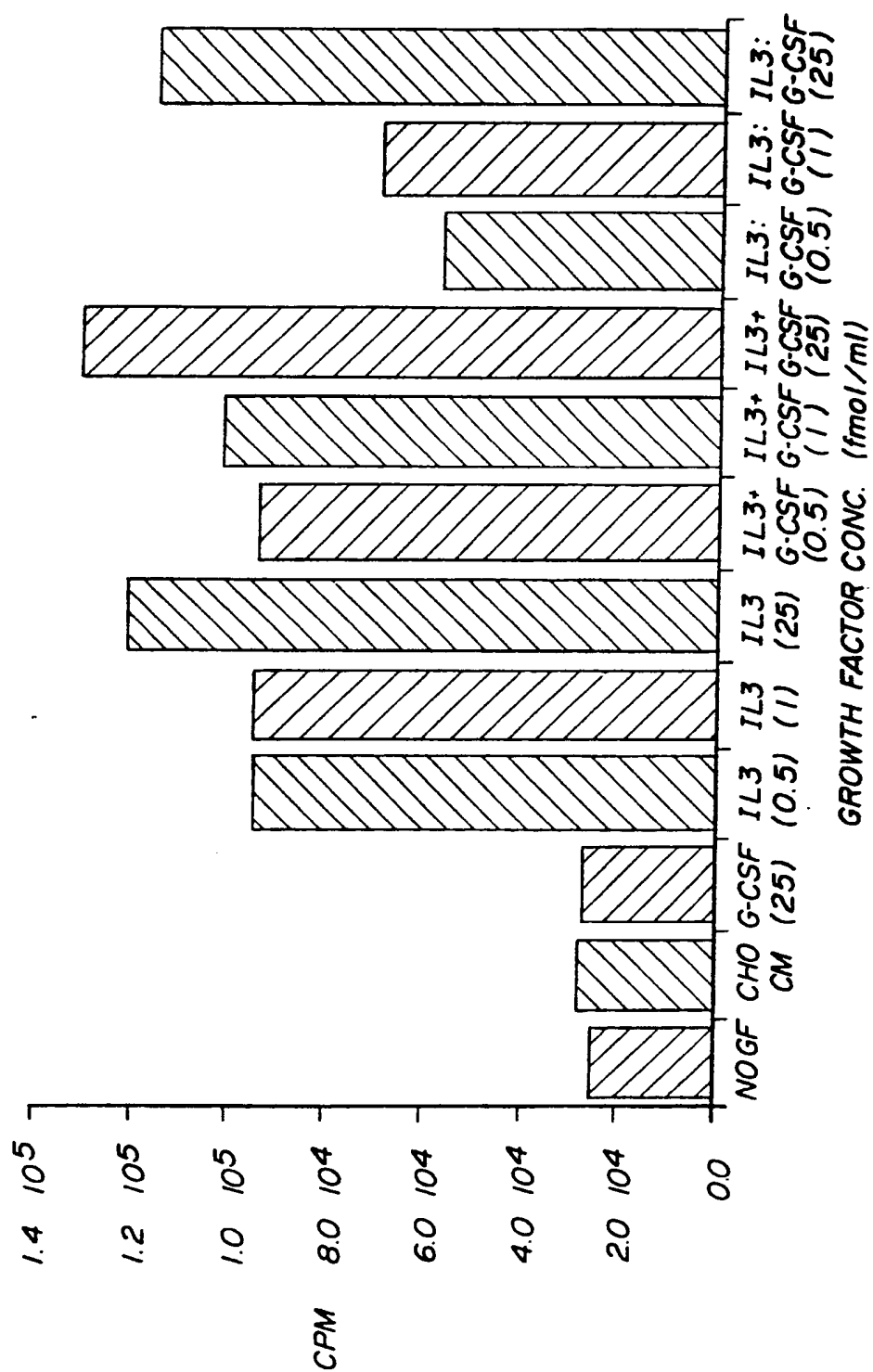
FIG-8B



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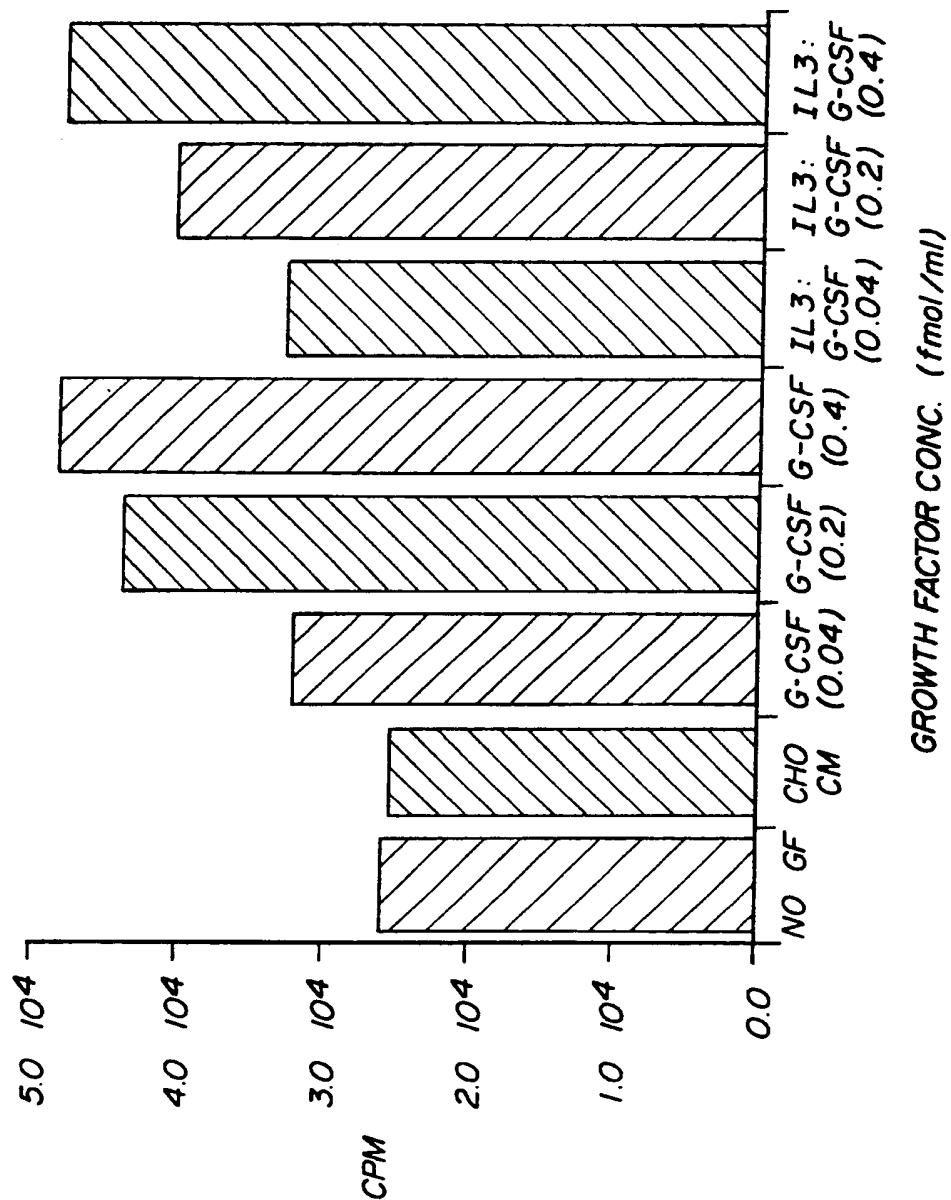
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FIG-9



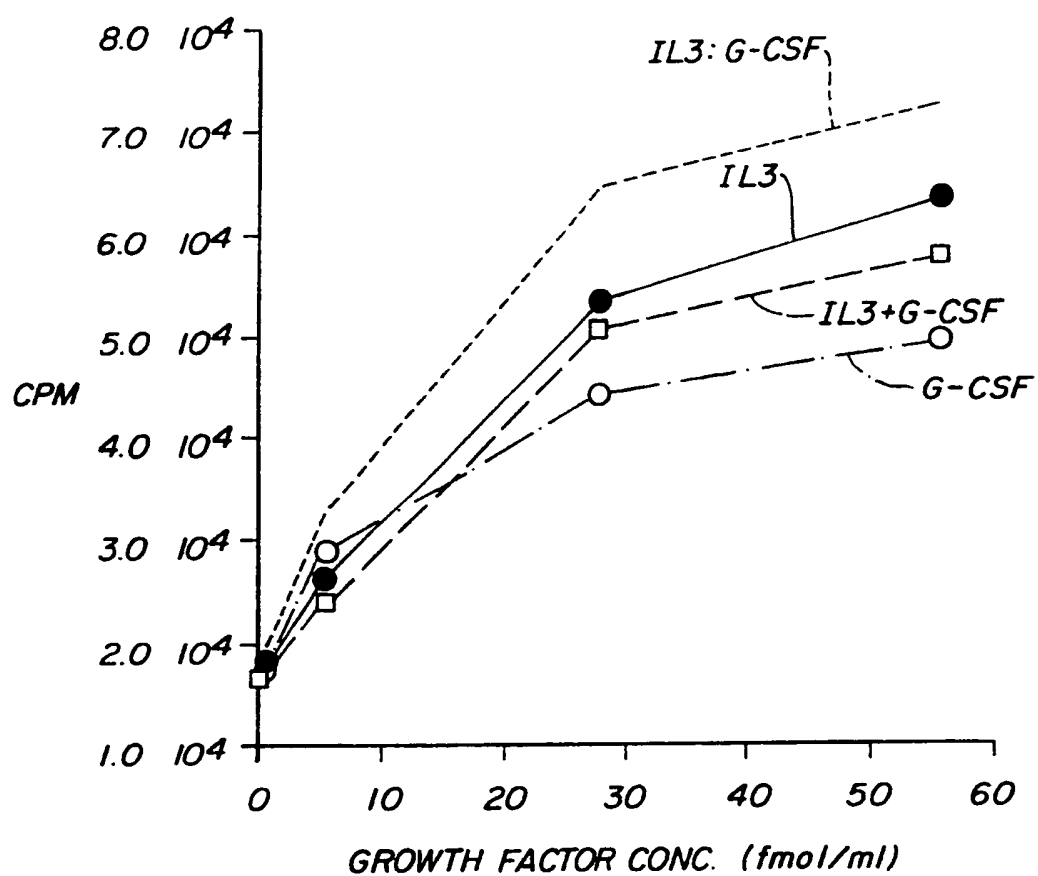
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FIG-10



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FIG-11



INTERNATIONAL SEARCH REPORT

International Application No. PCT/US91/07053

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all) ⁶ According to International Patent Classification (IPC) or to both National Classification and IPC IPC(5):007K 15/00; C12P21/02; C12N 15/24, 15/27, 15/70, 5/00, 5/10; A61K 37/02; 007H 15/12 U.S. CL.: 530/351,395;435/69.5,69.51,69.6,69.7, 172.3,240.1,320.1;424/85.1; 536/27						
II. FIELDS SEARCHED <div style="text-align: center; border: 1px solid black; padding: 2px; margin: 5px 0;">Minimum Documentation Searched ⁷</div> <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <th style="width: 20%;">Classification System</th> <th>Classification Symbols</th> </tr> <tr> <td style="text-align: center; vertical-align: top;">U.S.</td> <td>530/350,351,395; 435/69.1,69.5,69.51, 69.52, 69.6,69.7,172.3 240.1,252.3, 320.1; 424/85.1,85.2; 536/27</td> </tr> </table> <div style="text-align: center; border: 1px solid black; padding: 2px; margin: 5px 0;">Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched ⁸</div>			Classification System	Classification Symbols	U.S.	530/350,351,395; 435/69.1,69.5,69.51, 69.52, 69.6,69.7,172.3 240.1,252.3, 320.1; 424/85.1,85.2; 536/27
Classification System	Classification Symbols					
U.S.	530/350,351,395; 435/69.1,69.5,69.51, 69.52, 69.6,69.7,172.3 240.1,252.3, 320.1; 424/85.1,85.2; 536/27					
Computer Data-base search						
III. DOCUMENTS CONSIDERED TO BE RELEVANT ¹						
Category ⁹	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³				
E, <u>X</u> Y	US. A. 5,073,627 (Curtis et al.) 17 December 1991. see claims.	<u>1-2,20-26,4</u> 1-26				
Y	US. A. 4,935,233 (Bell et al.) 19 June 1990. see col. 3-4 and claims.	1-26				
Y	US. A. 4,935,352 (Koichi et al.) 19 June 1990. see all.	1-26				
P.Y	WO. A. 91/01004 (Svrluga et al.) 24 January 1991. see all.	1-26				
A	US. A. 4,675,382 (Murphy) 23 June 1987. see all.	1-26				
Y	WO. A. 88/00971 (Ramshaw et al.) 11 February 1988. see all.	1-26				
<div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> <p>¹⁰ Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="width: 45%;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"&" document member of the same patent family</p> </div> </div>						
IV. CERTIFICATION						
Date of the Actual Completion of the International Search 09 January 1992		Date of Mailing of this International Search Report <div style="font-size: 1.2em; font-weight: bold;">07 FEB 1992</div>				
International Searching Authority ISA/US		Signature of Authorized Officer <div style="text-align: center;"> Garnette D. Draper </div> <div style="text-align: right;">ebw</div>				